



Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan I.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
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 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

395										400					405				
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala					
				410					415					420					
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys					
				425					430					435					
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	Thr	His	Ser	Gly	Leu	Phe				
				440					445					450					
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr					
				455					460					465					
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu					
				470					475					480					
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg					
				485					490					495					
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val					
				500					505					510					
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu					
				515					520					525					
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly					
				530					535					540					
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr					
				545					550					555					
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu					
				560					565					570					
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val					
				575					580					585					
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr					
				590					595					600					
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys					
				605					610					615					
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe					
				620					625					630					
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln					
				635					640					645					
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe					
				650					655					660					
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Phe	Ser	Asp	Asp						
				665					670					675					
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala					
				680					685					690					

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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cccatgcgcc gccgcctctc cgcacgatgt tccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtec gggttgctct ccggcgccct 150
ccctcggaag tgttcgctct tccacctgtt cgtggcctgc ctctcgctgg 200
gctttctctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tggggccctc cccgtgectg 300
 cccccacagag ccgccccctg agcactggga agaagacgca tcttggggcc 350
 cccaccgect ggagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggtctctg tggccacat gcgccgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgagga gcagcaacag cacggactac 550
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 tgaacaggac aacctctcat ccccccaaa aaaaaaaaa aaaaaaaaa 1500
 aaaaaaaaa aaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

 <220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

 <220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

 <220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

 <220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

 <220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

 <400> 17
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 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

	140		145		150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp	155		160		165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala	170		175		180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His	185		190		195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His	200		205		210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly	215		220		225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu	230		235		240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe	245		250		255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg	260		265		270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly	275		280		285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu	290		295		300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp	305		310		315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser	320		325		

<210> 18

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 18

gcgaacgctt cgaggagtcc tgg 23

<210> 19

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24
 <223> Synthetic construct

 <400> 19
 gcagtgcggg aagccacatg gtac 24

 <210> 20
 <211> 46
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

 <400> 20
 cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

 <210> 21
 <211> 494
 <212> DNA
 <213> Homo sapiens

 <400> 21
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 aacgctgctg ctgctgctgc tgctgcttaa aggtcatgc ttggagtggg 100
 gactggctcg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
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 taacacgtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

 <210> 22
 <211> 73
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> sig_peptide
 <222> 1-15
 <223> Signal peptide.

 <220>
 <221> misc_feature
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
 1           5           10          15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
          20          25          30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
          35          40          45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
          50          55          60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctgggccgcg gccgcgctcc tgcccgcccg 150
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gaagaatggc tcattttctg ggtaaatctt cttgaaaga ttggacctcc 550
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<210> 24

<211> 616

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-33

<223> Signal peptide.

<220>

<221> TRANSMEM

<222> 13-40

<223> Transmembrane domain (type II).

<400> 24

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Leu	Leu	Pro	Leu	Ser	Leu	Leu	Ala	Leu	Leu	Ala	Leu	Leu	Gly	Gly	20	25	30	
Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His	35	40	45	
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	50	55	60	
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	65	70	75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	80	85	90	

Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	95	100	105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	110	115	120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	125	130	135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg	140	145	150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	155	160	165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	170	175	180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	185	190	195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	200	205	210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	215	220	225
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	230	235	240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	245	250	255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	260	265	270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	275	280	285
Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His	290	295	300
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln	305	310	315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg	320	325	330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser	335	340	345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp	350	355	360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln	365	370	375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro			

	380		385		390
Gln Asp Glu Arg	Lys 395	Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe 405	
Trp Ala Asp Asp	Asp 410	Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val 420	
Thr Arg Val Leu	Tyr 425	Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr 435	
Asn Ala Val Ala	Thr 440	Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu 450	
Ala Ala Asn Phe	Ser 455	Asp Lys Met Asp	Val Ile Phe Val Ala	Glu 465	
Met Ile Glu Lys	Phe 470	Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys 480	
Glu Leu Gly Asp	Val 485	Met Val Asp Ile	Ala Ser Asn Ile Met	Leu 495	
Ala Asp Glu Arg	Val 500	Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala 510	
Cys Ser Arg Ile	Val 515	Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg 525	
Leu Ala Gly Gly	Ala 530	His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile 540	
Ala Leu Glu Ala	Tyr 545	Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met 555	
Thr Cys Thr Val	Phe 560	Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly 570	
Leu Ser Asp Tyr	Gly 575	Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys 585	
Gln Leu Ser Phe	Lys 590	Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu 600	
Ala Leu Lys Val	Cys 605	Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr 615	

Ser

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25
gaggactcac caatctggtt cggc 24

<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
gtaaaggaga agaacatcac ggtacgggat accaggtgtg ttatactctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
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gcagagggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttggaac gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat ctcatcttt ttttttggtc 350
actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
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tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

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<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens
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 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

<400> 29
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 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
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<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
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 caccaccatc acaaccacca cgacgtcctc ttccggcctg gggcccccca 200
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 tctgtcttct cgtgacctg atcatctcca tcgtggagct gtgcgggtctc 400
 caggccccgt tccccctgtc ttggcgcaac ttccccatca ccttcgcctg 450

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 atgtccagtt cctgtcccac ggcggttcgc gggaccacgc catcgccgcc 550
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
				305					310					315	
His	Leu	Val	Phe	Val	Lys	Val									
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<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

<400> 32
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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
			20						25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
			35						40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
			50						55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
			65						70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
			80						85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
			95						100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
			110						115					120
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
			125						130					135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
			140						145					150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
			155						160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
			170						175					180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
			185						190					195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
			200						205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
			215						220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
			230						235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt ccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatccgc tcgcgatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
 <211> 23
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-23
 <223> Synthetic construct.

<400> 37
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<210> 38
 <211> 39
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-39
 <223> Synthetic construct.

<400> 38
 ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 39
 ctgctgcaaa gcgagcctct tg 22

<210> 40
 <211> 2084
 <212> DNA
 <213> Homo sapiens

<400> 40
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 tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
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 gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
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 gcattctttg ggcagtctaa aacccacatc taccatttcc acaagccctc 650
 ccttgatcca tagctttgtt tctaaagtgc ctggaatgc acctatagca 700
 gatgaagatc ttttgcccat ctacgcacat cccaatgcta cacctgtctc 750
 gtcttcagaa aacttcactt ggtcttttgt caatgacacc gtgaaaactc 800
 ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
 ccatctgtga ccccttgat agtggaacca agtggatggc ttaccacaaa 900
 cagtgatagc ttactgggt ttaccctta tcaagaaaaa acaactctac 950
 agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000
 gatcccaaaa aagaaaaatag aaatacagga atagtattcg gggccatttt 1050
 aggtgtctatt ctgggtgtct cattgcttac tcttggtggc tacttgttgt 1100
 gtggaaaaag gaaaacggat tcattttccc atcgcgact ttatgacgac 1150
 agaaatgaac cagttctgcg attagacaat gcaccggaac cttatgatgt 1200
 gagttttggg aattctagct actacaatcc aacttttgaat gattcagcca 1250
 tgccgaaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300
 cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350
 gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400
 ttacacaaaa ttactgtcac gtggtatttg tcaaggagaa tcataaaagc 1450
 aggagaccag tagcagaat gtagacagga tgtatcatcc aaaggttttc 1500
 tttcttaciaa tttttggcca tcctgaggca ttactaagt agccttaatt 1550
 tgtattttag tagtatttcc ttagtagaaa atatttgttg aatcagataa 1600
 aactaaaaga tttcaccatt acagccctgc ctacataacta aataataaaa 1650
 attattccac caaaaaatc taaaacaatg aagatgactc tttactgtct 1700
 tgctgaagc cctagtacca taattcaaga ttgcatttcc ttaaatgaaa 1750

attgaaaggg tgctttttaa agaaaatttg acttaaagct aaaaagagga 1800
 catagcccag agtttctggtt attgggaaat tgaggcaata gaaatgacag 1850
 acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
 gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
 aggaaagctg accctaccca ggaagtaat agcttcttta aaagtcttca 2000
 aagggttttg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050
 ttgggtgcct taaaaactca atgagaatca tggg 2084

<210> 41
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
 1 5 10 15
 Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
 20 25 30
 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
 35 40 45
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105
 Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
 110 115 120
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
 125 130 135
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
 140 145 150
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
 155 160 165
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
 170 175 180
 Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
 185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
 200 205 210
 Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
 215 220 225
 Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
 230 235 240
 Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
 245 250 255
 Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
 260 265 270
 His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
 275 280 285
 Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
 290 295 300
 Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
 305 310 315
 Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
 320 325 330
 Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgtag tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100
 ccctaccgc cgtgcaaaag gaggaggcgc ggcaagaagt ggaggccctc 150
 ctgagccga cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcattgccaa gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
 tctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgcc ctaatactt ctattgttat gcctccaaaa 600
 aatctggtag agctctttgg caaactggcg agtggcagat atctgcctca 650
 aacttatgtg gttcgagaag aacctagtgc tgtggaggaa attcgtgatg 700
 tttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtc 750
 ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800
 tgataaatgc tggagagatta gacacttccc caacgaattt attgttgaga 850
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtataa 900
 agaagtcaga gatttacaat atgactttaa cattaagggt tatgggatac 950
 tcaagatatt tactcatgca tttactctat tgcctatgct ttaaaaaag 1000
 gaaaaaaaaa aaaactacta accactgcaa gctcttgctc aattttatgt 1050
 taattggcat tgcttggttt ttgaaactga aattacatga gtttcatatt 1100
 ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
 cctaacaatcc tgacaataaa ttccatccgt tgtttttttt gtttgttgt 1200
 tttttctttt cctttaagta agctctttat tcactctatg gtggagcaat 1250
 tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaaa 1300
 tatcagatct caacattggt ggtttctttt gtttttcatt ttgtacaact 1350
 ttcttgaatt tagaaattac atctttgag ttctgttagg tgctctgtaa 1400
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaa 1500
 tgtgtagggt ctgaatgctg taaggagttt aggtgtgatg aattctacaa 1550
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
 1 5 10 15
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
 20 25 30
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
 35 40 45
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

	50		55		60
Ser Phe Ile Leu	Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr			
	65	70			75
Lys Tyr Phe Met	Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys				
	80	85			90
Phe Phe Asp Ser	Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu				
	95	100			105
Pro Asn Phe Leu	Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp				
	110	115			120
Asp Asn Ile Ala	Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp				
	125	130			135
Ser Asp Pro Ala	Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr				
	140	145			150
Ala Tyr Leu Asp	Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu				
	155	160			165
Asn Thr Ser Ile	Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe				
	170	175			180
Gly Lys Leu Ala	Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val				
	185	190			195
Arg Glu Asp Leu	Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn				
	200	205			210
Leu Gly Ile Phe	Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe				
	215	220			225
Arg Leu Arg Arg	Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala				
	230	235			240
Ile Asp Lys Cys	Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile				
	245	250			255
Val Glu Thr Lys	Ile Cys Gln Glu				
	260				

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 45
 gggaaactgct atctgatgcc 20

 <210> 46
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 46
 caggatctcc tcttgcatgc tgcagc 26

 <210> 47
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 47
 cttctcgaac cacataagtt tgaggcag 28

 <210> 48
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 48
 cagcattccc tccacagcaa ctggg 25

 <210> 49
 <211> 1969
 <212> DNA
 <213> Homo sapiens

 <400> 49
 ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggaactct ctcttcacgc ccaggtgccc cccactctcg ctccattcgg 100
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctcg gggcaccatg 150
 gtttcggcgg cagccccag cctctctatc ctctctgttc tgctgctggg 200
 gtctgtgctt gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
 tggagatgtt ggcgggtagt ggggaggcgg agggctcgtc ggectctcc 300
 ccgagcctcc cgccaccctg gaccccgccc ctacgcccc catcgatggg 350
 gcccagcccc acaaccctgg ggggccctac acccccacc aacttctgg 400
 atgggatatg ggaacttctc cgccagtacg tgatgtgat tgctgtgttg 450
 ggctccctgg cctttctgct gatgttcac gtctgtgcc cggtcatcac 500
 ccggcagaag cagaaggcct cggcctatta ccatcgctc tccccaaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggccccg ggcttctcgt 600
 gaggccccg acagagcccc cgacagcagg ccgagggaag ccttggtatc 650
 ctcccgccag ctccaggccc acatcttggc cgccaccag aacctcaagt 700
 cccccaccg ggctgcactg ggcgggtggg acggagccag gatggtggag 750
 ggagggggc cagaggaaga ggagaaggc agccaggagg gggaccagga 800
 agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850
 cgtgtccagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
 gagctggaag ggtctctctt gttagccag gaagccagg gaccagtggg 950
 tcccccgaa agccccgtg cttagcagcag tgctcaccac agtgtctaac 1000
 agtctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050
 ccccggtat gaaaaggcct tcagccctga ctgcttcctg acactccctc 1100
 cttggcctcc ctgtgtgtcc aatcccagca tgtgtgatt ctacagcagg 1150
 cagaaatgct ggtccccgtt gccccggagg aatcttacca agtgccatca 1200
 tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
 tgacaaaagt agggagggca cgtgtccctg tgacagccag gataaaacat 1300
 cccccaaagt gctgggatta caggcgtgag ccacogtgcc cgccccaaac 1350
 tactttttaa aacagctaca gggtaaaac ctgcagcacc cactctggaa 1400
 aatactgttc ttaattttcc tgaagggtgc cccctgttcc tagttgtccc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctcc 1500

caagcacc ccgctgggg gtgagtttct catcccgcta ctgctgctgg 1550
 gatcagggttg aatgaatgga actcttctctg tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtcga 1650
 ggggtgggg aagggtttct gacgccccagc ctggagcagg ggggccctgg 1700
 ccacccctctg ttgctcacac attgtctggc agcctgtgtc cacaatatct 1750
 gtcagtccctg gacagggagc ctgggctccg tctgtcttta gggaggtct 1800
 ggcaggaggt cctctccccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccagggtctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950
 aaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
				260					265					270	
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
				275					280						

<210> 51

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50

gacccagagg gaggaggac agggagtcgg aaggaggagg acaggaggag 100

gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150

agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200

cctggcctgc ctctgctgg ccctctgcct gggcagtggg gagcctggcc 250

ccctgcagag cgagaggagaa agcactggga caaatattgg ggaggccctt 300

ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350

caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttgccc 400

aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450

ggcgacagag atgctttggg caacagggtc ggggaagcag cccatgctct 500

gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550

acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600

ggtgcttggg aaacttctgg aggccatggc atctttgctc ctcaaggttg 650

ccttgaggcg cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcattgga gggccaccaa actttgggac 800
 caaacctcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gggcagcagc tggcggcagc 1050
 agtggtgga gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtctctc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggcttca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agaggggcaat cgcctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcagcgtg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcac 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag ccccccacat 1550
 cctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

	50		55		60
Gly Ala Ala Gly Ser	Lys Val Ser Glu	Ala Leu Gly Gln Gly Thr			
	65		70		75
Arg Glu Ala Val Gly Thr Gly Val Arg	Gln Val Pro Gly Phe Gly				
	80		85		90
Ala Ala Asp Ala Leu Gly Asn Arg Val	Gly Glu Ala Ala His Ala				
	95		100		105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg	Gln Ala Glu Asp Val				
	110		115		120
Ile Arg His Gly Ala Asp Ala Val Arg Gly	Ser Trp Gln Gly Val				
	125		130		135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser	Gly Gly His Gly Ile				
	140		145		150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln	Gly Gln Gly Asn Pro				
	155		160		165
Gly Gly Leu Gly Thr Pro Trp Val His Gly	Tyr Pro Gly Asn Ser				
	170		175		180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly	Ala Pro Trp Gly Gln				
	185		190		195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly	Thr Asn Thr Gln Gly				
	200		205		210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val	Arg Ala Ser Asn Gln				
	215		220		225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser	Gly Ser Gly Gly Gly				
	230		235		240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser	Gln Ser Gly Ser Ser				
	245		250		255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn	Gly Ser Ser Ser Gly				
	260		265		270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser	Ser Ser Ser Gly Gly Ser				
	275		280		285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly	Asn Ser Gly Gly Ser				
	290		295		300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp	Gly Ser Ser Thr Gly				
	305		310		315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly	Gly Gly Asn Gly His				
	320		325		330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu	Ala Arg Gly Ser Gly				
	335		340		345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
 350 355 360
 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
 365 370 375
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
 380 385 390
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
 395 400 405
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
 410 415 420
 Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
 425 430 435
 Ser Ser Arg Ile Pro
 440

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaccgggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggtcg 50
 caggcccgcc gggcgggtgct caccgtgccc tggtggtgg agtttctctc 100
 ctttctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct gcgcctgcac cggagcttgg tgtgtcgcga ggagagttag 200
 gggaagatgt gtttctgaa caagctgctg ctacttgctg tcctgggctg 250
 gcttttccag attccacag tccctgagga ctgttcttt ctggaagagg 300
 gtccctcata tgcccttgag gtggacacag tagcccccaga gcatggcttg 350
 gacaatgcgc ctgtggtgga ccagcagctg ctctacactc gctgccctca 400
 catcgagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450
 gacggagtgg gggcttcatg aggaaaaatca cccccaccac taccaccagc 500
 ctgggagccc agccttccca gaccagccag gggtgcagg cacagctcgc 550
 ccaggccttt ttccacaacc agccgccctc ctgcccgg accgtagagt 600
 tctgtgcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650
 ctggtggcag atctggtgcg ccaggcagag tcaactctcc aagagcagct 700
 ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750
 tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccttggggct gtgcggggcgc tgcttcaga 850
 ggagaccccgc gcagccgttc tgagcagtgcc agagaacatt gctgtggggc 900
 ttgcaacaga gaaagcctgt gcttggctgt cagccaacat cacagcactg 950
 atcaggaggag aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000
 tctgaacct gctgcccggg gggagcggag gggctgctcc cgcgcctgac 1050
 gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100
 agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150
 gccagttcct gtgccacct gctgagcagc atctggcaaa gtgctctgtg 1200
 gaggtagctt cctcctcgtg tgcagatcaa attcctatcc tagggcccc 1250
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Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr	Gln
	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val	Gln
	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln	Asp
	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys	Leu
	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro	Arg
	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly	Glu
	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser	Ser
	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg	Pro
	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val	Val
	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr	Ile
	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg	Leu
	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn	Cys
	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly	Arg

	560		565		570
Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile	Gln		
	575		580		585
Arg Asp Asp Pro	Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro	Asp			
	590		595		600
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr	Ile		
	605		610		615
Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro	Arg		
	620		625		630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr	Lys		
	635		640		645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala	Ile		
	650		655		660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys	Gly		
	665		670		675
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly	Glu		
	680		685		690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly	Tyr		
	695		700		705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile	Thr		
	710		715		720
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp	Met		
	725		730		735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe	Tyr		
	740		745		750
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr	Lys		
	755		760		765
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser	His		
	770		775		780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe	Asn		
	785		790		795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu	Thr		
	800		805		810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro	Pro		
	815		820		825
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu	Arg		
	830		835		840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu	Pro		
	845		850		855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 59
 gggaaacaca gcagtcattg cctgc 25

 <210> 60
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 60
 gcacacgtag cctgtcgtg gaggc 24

 <210> 61
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-42
 <223> Synthetic construct.

 <400> 61
 caccacaaag ccaggtccg gtacagcgtc aaacaagagt gg 42

 <210> 62
 <211> 1661
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 678
 <223> unknown base

 <400> 62
 cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50

 cgctgtctcc tcccaggctc ccgcggccga cccccgcga acatgcagcc 100

 cagggcgccg gagggttccc gcgcgctcag ccggcggtat ctgcggcgtc 150

 tgctgtctct gctactgtg ctgctgtcgc ggcagcccg aaccgcgcg 200

 gagaccacgc cggcgcccc cagagccctc tccacgctgg gctccccac 250

 cctcttcacc acgcccgggtg tcccagcgc cctcactacc ccaggctcca 300

 ctacgccagg caccaccaaa accctggacc ttccggggtcg cgcgcaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
 cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
 tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
 gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagatgc 550
 cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
 cctactctga actcagagctt gtgacctcag ctgaaggtct gaacagctct 650
 caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
 cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
 cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
 agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850
 agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
 catcggacac cttgataaga agggctcttg aagtgtctca ggctcctgtg 950
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 tcccgatgat atcctgcagc ttctgaagaa cggtggcata gtgatgtgta 1050
 cactgtccat gggggtgctg cagtgcaccc tgccttctaa cgtgtccact 1100
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
 cgggattggt ggaaattatg acgggaactg ccggttccct caggggctgg 1200
 aggatgtgtc cacataccca gtctgatag aggagttgct gagtcgtasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcaggcgc cagagccccg 1350
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400
 ctgctgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaccaat cgggtccctt ggaggtcctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggtgct gccaccatcc caaccttacc ccagtggctc 1550
 tgcgtacaca gtcgtccccc gcagaggtea ctgtggcaaa gcctcacaaa 1600
 gcccccctct ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
1				5					10					15	
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu	Glu Val Ser Gln Ala Pro	
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg	Ala Val Cys Asp Asn Leu	
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly Gly	
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly	Val Leu Gln Cys Asn Leu	
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp	His Phe Asp His Ile Arg	
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr Asp	
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr Tyr	
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu Glu	
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn	Leu Leu Arg Val Phe Arg	
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro Val	
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His Ser	
425	430	435
His Leu Val Pro Gln Asn Gly His Gln	Ala Thr His Leu Glu Val	
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn Ala	
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val	Ala Ala Ala Thr Ile Pro	
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 66
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens

<400> 67
 tgctaggctc tgtccacaa tgcacccgag agcaggagct gaaagcctct 50
 aacacccaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100
 ggccagcaa gctgataag catgaagctc ttatctttgg tggctgtggt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcatctgt ccacctata gaaacatcag tgggcacatt 250
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
 gcccatgccca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
 agtgacggtg cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
 atctacctgt ccgtggtggg tgcctgttg ctctacatgg ccttcctgat 450
 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
 acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
 tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650
 atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacacccat ggctgccagc ttccaggtcg gacaaagcag ggggctactt 750
 ctcccttccc tcggttcagc tcttcccttt aaaagcctgt ggcatttttc 800
 ctctctctcc ctaacttttag aaatgttgta ctggctatt ttgattaggg 850
 aagagggatg tggctctcga tctctgttgt ctcttgggt ctttggggtt 900
 gaagggaggg ggaaggcagc ccagaaggga atggagacat tcgaggcggc 950
 ctccaggagt gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
 cagctctgag tcttgggaat gttgttacc ttggaagata aagctgggtc 1050
 ttcaggaact cagtgtcttg gaggaagca tggcccagca ttcagcatgt 1100
 gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150
 ctccagccca gccccagctc cagccctgag gacagctctg atgggagagc 1200
 tggggccctc gagcccaact ggtcttcagg gtgcactgga agctggtgtt 1250
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 ctctgtgcc ggctccctca cctgcacttg aggggtcttg gcagtccttc 1350
 ctctccccc tgccacagc cactgagcca gacggtcgtt tggaacatga 1400
 gactcgagcg tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tcctcttgtc tttagattgt gtgtaaatca aggaagccat cattaatttg 1550
 ttttattttc ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Ala	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
				170					175					180	

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttgggttc cgctaatttc tgcctgagc cgtgagactg 50
 agttcatagg gtctgggttc ccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggctctccc 150
 tccctttgca tcccacccc tccgggcttt gcgtcttct ggggaacccc 200
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgtctgcc 250
 tgctctact ggccgcgtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggccca aactcaact catcaagtcc tctctggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcgt gtaccaagga ctggcattcg 400
 gcggcagtaa gaagggcataaacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcacc accaaggatc 500
 atcgccctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
 gcattgtctg ccccgatacc cgctgcaata atggcatctg tatcccgatt 600
 actgaaagca tcttaacccc tcacatcccc gctctggatg gtactcgcca 650

cagagatcga aaccacggc attactcaaa ccatgacttg ggatggcaga 700
 atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
 gacccctgcc tacgatcacc agactgcatt gaagggtttt gctgtgctcg 800
 tcatttcttg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
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 ctctcccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
 ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
 catggtggaa aataagggtc agatgcagaa gaatggctaa aataagaaac 1100
 gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
 aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
 caacttgtct atgtaataaa tgtacacatt tgtgaaaaa gctattatta 1250
 agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
 aagagtttag gttgtgctgg aggagaggtt tccttcagat tgcgtattgc 1350
 ttatacaaat aacctacatg ccagattttct attcaacgtt agagttaa 1400
 aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaatt 1450
 gctaacaacg aatgaaaac atggagcatt gtaatttac aacagaaaa 1500
 taccttttga ttgttaacac tacttctgct gttcaatcaa gagtcttggt 1550
 agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
 cagttgttta ggaaggcctt taggaagaca aataataac aaacaaacag 1650
 ccacaatac ttttttttca aaatttttagt ttacctgtga attaataaga 1700
 actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
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 aactataccc ataaattgtg actagtaaaa tacttacaca gacgagaatt 1850
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 gctaacagag agatcattat ttcttaaga ttggccataa cctatatttt 1950
 gatagaatta gattggtaaa tacatgtatt catacactat ctgtggtaat 2000
 agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
 aaaacttttt cgtttgttca ggttttgca acacatagat catatgtctg 2100

aggcacaagt tggtctgttca tctttgaaac caggggatgc acagtctaaa 2150
 tgaataatctg catgggattt gctatcataa tatttactat gcagatgaat 2200
 tcagtgtgag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250
 tgctgagatc ctcaaaatat ctcaatttca ggaggtttca caaaatgtac 2300
 tcctgaagta gacagagtag tgaggtttca ttgccctcta taagcttctg 2350
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 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
 acccagcttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550
 aactcagttc taaatacttt gtctggagca caaaacaata aaagggtatc 2600
 ttatagtcgt gactttaaac tttttagagc cacaattcac ttttagttt 2650
 tcttttactt aaatccatc tgcagctcca aatttaagtt ctcccagtag 2700
 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
 tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
 caaaaattat aaactagtcc atccaagaac caaagtttgt ataacagggt 2850
 tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900
 atataacaat tattatattt acaatttggg ttctgcaata ttttcttat 2950
 gtccaccctt ttaaaaatta tttttgaag taatttattt acaggaaatg 3000
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
 taagataaaa tctattaaat ttttctcttc taaaaactga aaaaaaaaaa 3150
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20				25					30	
Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
			35					40					45	

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	
				50					55					60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	
				65					70					75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	
				80					85					90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	
				95					100					105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	
				110					115					120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	
				125					130					135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	
				140					145					150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	
				155					160					165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	
				170					175					180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	
				185					190					195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	
				200					205					210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	
				215					220					225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	
				230					235					240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	
				245					250					255	

Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
 tctcaatctg ctgacctcgt gatccgcctg accttgtaat ccacctacct 50
 tggcctccca aagtgttggg attacaggcg tgagccaccg cgccccggcca 100
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatattt catgtagtat ttctaaagt 250
 atatttttagt aattcatatg ttttagatta taggttttaa catacttg 300
 aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgtga 350
 ggatttgttc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400
 tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
 tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggag 550
 ctcaagcccc caacatccca gtctcagtc ctcagtcac ttgacttcaa 600
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaa 650
 agcaccagag ccaggcagtc actgttctct ctcctggttt ggagtccttt 700
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
 tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800
 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
 atacccccag ctctaaagt cccagcttct gcagtggaat tgcctgtgtc 900
 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950
 cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000
 aatcagattc ccatcagctt gtattcgaag tctttaagt agcctttgaa 1050
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100
 ccgtcattac ctctgcagtc ctgacaagct catcactgaa ttctgctagt 1150
 ccagtagcaa tgtcttctc ttatgaccag agttctgtgc ataacaggat 1200
 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
 tgaatggaca tgggtgtgtt cgaagtcagc agacactaga cagtaagtat 1300
 agcagcaagc tactcttgtc atggctgtgt ccaaccaaac agagggaagag 1350
 gatagctcac gtgatgtgga aaacaccagt tggccaatgg ctcaattcgtt 1400
 aaaagcagc ccttttgctt ttttgtttt ggaccaggtg ttggtctgtg 1450
 tgttattaga aatgtcttaa ccacagcaag aaggaggtgg tggctctata 1500
 ttctctgtcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
 tttaaagatg cttgggccag gcgggggtggc tgatgcccat aatcccagtg 1600
 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
 gccgggtgtg gtggcggcgc gtgcctgtaa tccagctac ttgggaggct 1750
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
 ctgaaaaga 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
 1 5 10 15
 Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
 20 25 30
 Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
 35 40 45
 Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
 50 55 60
 Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
 65 70 75
 Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
 80 85 90
 Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
 95 100 105
 Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
 110 115 120
 Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
 125 130 135
 Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
 140 145 150
 Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
 155 160 165
 Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 170 175 180
 Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
 185 190 195
 Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
 200 205 210
 Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.
 <400> 73
 aattcatggc aaatatttcc cttecc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.
 <400> 74
 tggtaaactg gcccaaactc gg 22
 <210> 75
 <211> 50

<212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct

 <400> 75
 ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccacccaa 50

 <210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

 <400> 76
 gccgagtgagg acaaagcctg gggctggggc ggggccatgg cgcctgccatc 50
 ccgaatcctg ctttggaaac ttgtgcttct gcagagctct gctgttctcc 100
 tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
 caccatcact actgccacct ctacgagagc ctggccgtcc gcctggaggt 200
 caccgacggc cccccggcca cccccgcta ctgggacggc gagaaggagg 250
 tgcctggcgtt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
 gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350
 ctgggaccgg cagccgcccg ggggtcccga cgaccgcgcg gaccgcctgc 400
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 gccacaagct catcaatgtc atcgtccccg agagccgagc ccactttctc 750
 cagcagctgg gctacgtgct ggccacgctg ctgctcttca tctgctact 800
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 cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900
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 gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
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cagcccaaaa actgggtgca gcctcagggc agggagtccca ctctccagg 1450
gctctgctgc tccggggctg ggagatgttc ctggaggagg acactcccat 1500
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tggtcgagga caggggaggg agtgaagtgg gtttggggg gcctgtgttg 1900
ccactctcag caccacacat ttgcactctgc tgggtggacct gccaccatca 1950
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
1 5 10 15
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala	Pro Ala Leu Leu Thr	Cys Val Asn Arg Gly His
80		90
Val Trp Thr Asp	Arg His Val Glu Glu Ala	Gln Gln Val Val His
95		105
Trp Asp Arg Gln	Pro Pro Gly Val Pro	His Asp Arg Ala Asp Arg
110		120
Leu Leu Asp Leu	Tyr Ala Ser Gly Glu Arg	Arg Ala Tyr Gly Pro
125		135
Leu Phe Leu Arg	Asp Arg Val Ala Val	Gly Ala Asp Ala Phe Glu
140		150
Arg Gly Asp Phe	Ser Leu Arg Ile Glu	Pro Leu Glu Val Ala Asp
155		165
Glu Gly Thr Tyr	Ser Cys His Leu His	His Tyr Cys Gly Leu
170		180
His Glu Arg Arg	Val Phe His Leu Thr	Val Ala Glu Pro His Ala
185		195
Glu Pro Pro Pro	Arg Gly Ser Pro Gly	Asn Gly Ser Ser His Ser
200		210
Gly Ala Pro Gly	Pro Asp Pro Thr Leu	Ala Arg Gly His Asn Val
215		225
Ile Asn Val Ile	Val Pro Glu Ser Arg	Ala His Phe Phe Gln Glu
230		240
Leu Gly Tyr Val	Leu Ala Thr Leu Leu	Leu Phe Ile Leu Leu Leu
245		255
Val Thr Val Leu	Leu Ala Ala Arg Arg	Arg Arg Gly Gly Tyr Glu
260		270
Tyr Ser Asp Gln	Lys Ser Gly Lys Ser	Lys Gly Lys Asp Val Asn
275		285
Leu Ala Glu Phe	Ala Val Ala Ala Gly	Asp Gln Met Leu Tyr Arg
290		300
Ser Glu Asp Ile	Gln Leu Asp Tyr Lys	Asn Asn Ile Leu Lys Glu
305		315
Arg Ala Glu Leu	Ala His Ser Pro Leu	Pro Ala Lys Tyr Ile Asp
320		330
Leu Asp Lys Gly	Phe Arg Lys Glu Asn	Cys Lys
335		340

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78
 cgccggaggc agcggcggcg tggcgagcg gcgacatggc cgttgtctca 50
 gaggaagact ttcagcacag ttcaaaactcc acctacggaa ccacaagcag 100
 cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150
 cggcccttg cctgcagagg ccgaggagcc gcttctgtgg cacatacatc 200
 atctttctca gcctgggcat tggcagtgta ctgccatgga acttctttat 250
 cactgccaag gactactgga tgttcaaaact ccgcaactcc tccagcccag 300
 ccacggggga ggaccctgag ggctcagaca tctgaacta ctttgagagc 350
 taccttgccg ttgcctccac cgtgccctcc atgctgtgac tggtgcccaa 400
 ctctctgctt gtcaacaggg ttgcagtcca catccgtgac ctggcctcac 450
 tgacggctcat cctggccatc ttcatgggtg taactgcact ggtgaagggtg 500
 gacacttctc cctggaccgg tgggtttttt gcgggtcacca ttgtctgcat 550
 ggtgatcttc agcgggtgct ccactgtctt cagcagcagc atctacggca 600
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 gccatggggc ggacggtcag gcgcgtggcc tcattgggtg acttgctgctc 700
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 tcttctctgt gctctgcatg ggaactctacc tgctgctgac caggctggag 800
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 gccagcctgg gcttctgtgt caactacgtc ttcttcatca ccagcctcat 1000
 ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050
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 aactttgtcg acctatgtg ccggcagctc accgcctgga tccaggtgcc 1150
 agggcccaac agcaaggcgc tccagggtt cgtgctctc cggacctgcc 1200
 tcatccccct cttcgtgctc tgtaactacc agcccccgct ccacctgaag 1250
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 ggggctcagc aacggctacc tcagaccctt ggccctctc tacgggccta 1350
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 tatgtgtgct tgggcttaac actgggctca gcctgctcta cctcctggt 1450

gcacctcate tagaaggag gacacaagga cattggtgct tcagagcctt 1500
 tgaagatgag aagagagtgc aggagggctg ggggccatgg aggaaagccc 1550
 taaagtttca cttggggaca gagagcagag cacactcggg cctcaccct 1600
 cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650
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 ttctagccct tcaaagatgc tgccagtgtt cgcctagag ttattacaaa 1800
 gccagtgccaa aaaccagacc atgggctctt tgcaacctcc cagctgcgct 1850
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 gaaggggtct ccttgaatg gaagtcccct ggcctgggtc gtcctcagcg 1950
 ccaagactca agtgtgcaca gaccctctgt ttctcgggtt gaacaactgc 2000
 ccactaacca gactggaaaa ccagaaaaga tgggccttcc atgaatgctt 2050
 cattccagag ggaccagagg gcctccctgt gcaagggtc aagcatgtct 2100
 ggcctgggtt ttcaaaaaa gagggatcct catgacctgg tggctctatgg 2150
 cctgggtcaa gatgaggtc ttctagtgtt cctgtttaca acatgtcaaa 2200
 gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	
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Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	
				20					25					30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Gly	Leu	Gln	Arg		
				35				40					45		
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	
				50					55				60		
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	
				65				70						75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	
				80				85						90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	
				95					100					105	

Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

	395	400	405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser	Ser
	410	415	420
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu	Leu
	425	430	435
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr	Gly
	440	445	450
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly	Ser
	455	460	465
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile	
	470	475	

<210> 80

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 80

ttttgcggtc accattgtct gc 22

<210> 81

<211> 23

<212> DNA

<213> Homo sapiens

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 81

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<210> 82

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-49

<223> Synthetic construct.

<400> 82

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<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
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 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
 200 205 210
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
 215 220 225
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
 230 235 240
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
 245 250 255
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
 260 265 270
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
 275 280 285
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
 290 295 300
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
 305 310 315
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
 320 325 330
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
 335 340 345
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
 350 355 360
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
 365 370 375
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 380 385 390
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
 395 400 405
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
 410 415 420
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
 425 430 435
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
 440 445 450
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
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<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
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aatttttgta cagggggaga gcttacggtc atccttagta ggagtgggtg 2000
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 aactgatctc cccaccctt ggattagagt tctgtctcta ccttaccac 3250
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 tattacagat aaaaaa 3316

<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

Gly Ser Pro His	Ser	Leu Glu Ala Leu Arg	Asp Ala Ala Pro Ser	35	40	45
Gln Gly Leu Asn	Phe	Leu Leu Leu Phe Thr	Lys Met Leu Phe Ile	50	55	60
Phe Asn Phe Leu	Phe	Ser Pro Leu Pro Thr	Pro Ala Leu Ile Cys	65	70	75
Ile Leu Thr Phe	Gly	Ala Ala Ile Phe	Leu Trp Leu Ile Thr Arg	80	85	90
Pro Gln Pro Val	Leu	Pro Leu Leu Asp	Leu Asn Asn Gln Ser Val	95	100	105
Gly Ile Glu Gly	Gly	Ala Arg Lys Gly	Val Ser Gln Lys Asn Asn	110	115	120
Asp Leu Thr Ser	Cys	Cys Phe Ser Asp	Ala Lys Thr Met Tyr Glu	125	130	135
Val Phe Gln Arg	Gly	Leu Ala Val Ser	Asp Asn Gly Pro Cys Leu	140	145	150
Gly Tyr Arg Lys	Pro	Asn Gln Pro Tyr	Arg Trp Leu Ser Tyr Lys	155	160	165
Gln Val Ser Asp	Arg	Ala Glu Tyr Leu	Gly Ser Cys Leu Leu His	170	175	180
Lys Gly Tyr Lys	Ser	Ser Pro Asp Gln	Phe Val Gly Ile Phe Ala	185	190	195
Gln Asn Arg Pro	Glu	Trp Ile Ile Ser	Glu Leu Ala Cys Tyr Thr	200	205	210
Tyr Ser Met Val	Ala	Val Pro Leu Tyr	Asp Thr Leu Gly Pro Glu	215	220	225
Ala Ile Val His	Ile	Val Asn Lys Ala	Asp Ile Ala Met Val Ile	230	235	240
Cys Asp Thr Pro	Gln	Lys Ala Leu Val	Leu Ile Gly Asn Val Glu	245	250	255
Lys Gly Phe Thr	Pro	Ser Leu Lys Val	Ile Ile Leu Met Asp Pro	260	265	270
Phe Asp Asp Asp	Leu	Lys Gln Arg Gly	Glu Lys Ser Gly Ile Glu	275	280	285
Ile Leu Ser Leu	Tyr	Asp Ala Glu Asn	Leu Gly Lys Glu His Phe	290	295	300
Arg Lys Pro Val	Pro	Pro Ser Pro Glu	Asp Leu Ser Val Ile Cys	305	310	315
Phe Thr Ser Gly	Thr	Thr Gly Asp Pro	Lys Gly Ala Met Ile Thr			

	320		325		330
His Gln Asn Ile	Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val			
	335		340		345
Glu His Ala Tyr	Glu Pro Thr Pro Asp Asp	Val Ala Ile Ser Tyr			
	350		355		360
Leu Pro Leu Ala	His Met Phe Glu Arg	Ile Val Gln Ala Val Val			
	365		370		375
Tyr Ser Cys Gly	Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg			
	380		385		390
Leu Leu Ala Asp	Asp Met Lys Thr Leu Lys	Pro Thr Leu Phe Pro			
	395		400		405
Ala Val Pro Arg	Leu Leu Asn Arg Ile Tyr	Asp Lys Val Gln Asn			
	410		415		420
Glu Ala Lys Thr	Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val			
	425		430		435
Ser Ser Lys Phe	Lys Glu Leu Gln Lys Gly	Ile Ile Arg His Asp			
	440		445		450
Ser Phe Trp Asp	Lys Leu Ile Phe Ala Lys	Ile Gln Asp Ser Leu			
	455		460		465
Gly Gly Arg Val	Arg Val Ile Val Thr Gly	Ala Ala Pro Met Ser			
	470		475		480
Thr Ser Val Met	Thr Phe Phe Arg Ala Ala	Met Gly Cys Gln Val			
	485		490		495
Tyr Glu Ala Tyr	Gly Gln Thr Glu Cys Thr	Gly Gly Cys Thr Phe			
	500		505		510
Thr Leu Pro Gly	Asp Trp Thr Ser Gly His	Val Gly Val Pro Leu			
	515		520		525
Ala Cys Asn Tyr	Val Lys Leu Glu Asp Val	Ala Asp Met Asn Tyr			
	530		535		540
Phe Thr Val Asn	Asn Glu Gly Glu Val Cys	Ile Lys Gly Thr Asn			
	545		550		555
Val Phe Lys Gly	Tyr Leu Lys Asp Pro Glu	Lys Thr Gln Glu Ala			
	560		565		570
Leu Asp Ser Asp	Gly Trp Leu His Thr Gly	Asp Ile Gly Arg Trp			
	575		580		585
Leu Pro Asn Gly	Thr Leu Lys Ile Ile Asp	Arg Lys Lys Asn Ile			
	590		595		600
Phe Lys Leu Ala	Gln Gly Glu Tyr Ile Ala	Pro Glu Lys Ile Glu			
	605		610		615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
			620						625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
			635						640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
			650						655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
			665						670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
			680						685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
			695						700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
			710						715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 ccaggacatt ggtgacccgc caatccgta tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 cagggggccgt gcttttctctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctcgcgagc catcagtga gccaatgaag acccagagcc 350
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 gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450
 agcaaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
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 cctgtctgag gaggctgggc agccaggctg gccctgccct gggtggagg 750
 gacacatggg ccttcgtggg acgaaaagga ggtcctgtct tcggggagaa 800
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 gacacagagc tgaaccgtcg ccgcccggcg tctgcagca aagttgaggg 950
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 ttctggaaga ggacctggac attgtctgtg attttttcag tttctgagc 1350
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<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
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 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
 140 145 150
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
 155 160 165
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
 170 175 180
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
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 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
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 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
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 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
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 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
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 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
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 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
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Ser Arg Ser Tyr	His Phe Gly Ile Val Gly	Leu Asn Met Asn Gly	
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Tyr Phe His Glu	Ala Tyr Phe Lys Lys His	Lys Phe Asn Thr Val	
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Pro Gly Val Gln	Leu Arg Asn Val Asp Ser	Leu Lys Lys Glu Ala	
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Tyr Glu Val Glu	Val His Arg Leu Leu Ser	Glu Ala Glu Val Leu	
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Asp His Ser Lys	Asn Pro Cys Glu Asp Ser	Phe Leu Pro Asp Thr	
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Glu Gly His Thr	Tyr Val Ala Phe Ile Arg	Met Glu Lys Asp Asp	
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Asp Phe Thr Thr	Trp Thr Gln Leu Ala Lys	Cys Leu His Ile Trp	
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Asp Leu Asp Val	Arg Gly Asn His Arg Gly	Leu Trp Arg Leu Phe	
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Arg Lys Lys Asn	His Phe Leu Val Val Gly	Val Pro Ala Ser Pro	
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<400> 89

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 <212> DNA
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<400> 94

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 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
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 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
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 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
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 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
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 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
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 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
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 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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				Thr	Phe
					Leu
					255
Tyr	Val	Ala	Thr	Val	His
	260	Val	Leu	Pro	Glu
				Val	Gly
				Gly	Ile
					Gly
					270
His	Ser	His	Lys	Pro	Asp
	275	Ala	Thr	Gly	Gly
				Arg	Gly
				Leu	Ser
					Arg
					285
Leu	Glu	Val	Ala	Ala	Leu
	290	Val	Leu	Gly	Cys
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					Ile
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<400> 97
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<210> 98
 <211> 50
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 <213> Artificial

<220>
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<210> 99
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<212> DNA

<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
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Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
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<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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 acagagagtg ctggagaaca gtgtagcctg gcctgtacag gtactggatg 3350
 atctgcaaga caggctcagc catactctta ctatcatgca gccaggggcc 3400

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450
 tgatccctaa ctctgattt ggaatgcattt gagggacaag gggggcggtc 3500
 tccgaagtgg aataaaatag gccgggcgtg gtgacttgca cctataatcc 3550
 cagcactttg ggaggcagag gtgggaggat tgcttggtcc caggagtcca 3600
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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe
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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
				20					25					30
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
				35					40					45
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50					55					60
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
				65					70					75
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80					85					90
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
				95					100					105
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110					115					120
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125					130					135
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140					145					150
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
				155					160					165
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
				170					175					180
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
				185					190					195
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

	200	205	210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
500	505		510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515	520		525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530	535		540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu	Phe
545	550		555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560	565		570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575	580		585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590	595		600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605	610		615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620	625		630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635	640		645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650	655		660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665	670		675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Glu
680	685		690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695	700		705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710	715		720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725	730		735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740	745		750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755	760		765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770	775		780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
	800	805	810
Arg Leu Glu Arg Thr	Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
	815	820	825
Tyr Gln Leu Gly Ser	Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
	830	835	840
Thr Leu Leu Ala Phe	Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
	845	850	855
Ser Leu Val Phe Leu	Leu Leu Phe Leu	Ser Phe Leu Leu Leu	
	860	865	870
His Leu Leu Ala Ala	Gly Ile Pro Val Thr	Thr Pro Gly Pro Phe	
	875	880	885
Thr Val Pro Trp Gln	Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
	890	895	900
Gln Thr Phe Tyr Ser	Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
	905	910	915
His Trp His Ala Ala	Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
	920	925	930
Cys Thr Trp Leu Pro	Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
	935	940	945
Ser His Leu Leu Phe	Ala Val Gly Cys	Pro Leu Leu Leu Trp	
	950	955	960
Pro Phe Leu Cys Glu	Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
	965	970	975
Pro Gly Asn Glu Ala	Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
	980	985	990
Glu Pro Leu Met Glu	Met Arg Leu Arg Asp	Ala Pro Gln His Phe	
	995	1000	1005
Tyr Ala Ala Leu Leu	Gln Leu Gly Leu Lys	Tyr Leu Phe Ile Leu	
	1010	1015	1020
Gly Ile Gln Ile Leu	Ala Cys Ala Leu Ala	Ala Ser Ile Leu Arg	
	1025	1030	1035
Arg His Leu Met Val	Trp Lys Val Phe Ala	Pro Lys Phe Ile Phe	
	1040	1045	1050
Glu Ala Val Gly Phe	Ile Val Ser Ser Val	Gly Leu Leu Leu Gly	
	1055	1060	1065
Ile Ala Leu Val Met	Arg Val Asp Gly Ala	Val Ser Ser Trp Phe	
	1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgtgcc gccgtgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgcc aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtcatt tctgttgccc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tctgtttccc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatcaaac agaacgtggt ccagtggtg gaccaaccac acgctgggtc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttgacaaa gagaacacac cagcaaatat 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcaccccca atatctcgga tgattctaaa 750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccctc caggagggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctc 950
cagcagaaca atacccccg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgccacaca aggaacatta ttgagtcgc aggcagcgtt 1100
ggcagtcctg ggcccgcaaa cgttacagta ctacacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200
gagggaagag catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
 agccttctga ggggatggg ctcggagagg aggtctctt atctagactc 1350
 tatgaggagc cggtccaga caggccacca ggagaaaatg aaacctatct 1400
 catcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450
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 cctttgatcc cagccataaa gtacctggga tgaagaagt ttttccagt 1550
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 cgtgtgtgat tggttcatgc atgtaggtct ctaacaatg atgggtggcc 1650
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 aatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
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 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly	Lys Glu Lys His Pro	Ala Asn Leu Ile Leu	Ile
	170	175	180
Tyr Gly Asn Glu	Phe Asp Lys Arg Phe	Phe Val Pro Ala Glu	Lys
	185	190	195
Ile Val Ile Asn	Phe Ile Thr Leu Asn	Ile Ser Asp Asp Ser	Lys
	200	205	210
Ile Ser His Gln	Asp Met Ser Leu Leu	Gly Lys Ser Ser Asp	Val
	215	220	225
Ser Ser Leu Asn	Asp Pro Gln Pro Ser	Gly Asn Leu Arg Pro	Pro
	230	235	240
Gln Glu Glu Glu	Glu Val Lys His Leu	Gly Tyr Ala Ser His	Leu
	245	250	255
Met Glu Ile Phe	Cys Asp Ser Glu Glu	Asn Thr Glu Gly Thr	Ser
	260	265	270
Leu Thr Gln Gln	Glu Ser Leu Ser Arg	Thr Ile Pro Pro Asp	Lys
	275	280	285
Thr Val Ile Glu	Tyr Glu Tyr Asp Val	Arg Thr Thr Asp Ile	Cys
	290	295	300
Ala Gly Pro Glu	Glu Gln Glu Leu Ser	Leu Gln Glu Glu Val	Ser
	305	310	315
Thr Gln Gly Thr	Leu Leu Glu Ser Gln	Ala Ala Leu Ala Val	Leu
	320	325	330
Gly Pro Gln Thr	Leu Gln Tyr Ser Tyr	Thr Pro Gln Leu Gln	Asp
	335	340	345
Leu Asp Pro Leu	Ala Gln Glu His Thr	Asp Ser Glu Glu Gly	Pro
	350	355	360
Glu Glu Glu Pro	Ser Thr Thr Leu Val	Asp Trp Asp Pro Gln	Thr
	365	370	375
Gly Arg Leu Cys	Ile Pro Ser Leu Ser	Ser Phe Asp Gln Asp	Ser
	380	385	390
Glu Gly Cys Glu	Pro Ser Glu Gly Asp	Gly Leu Gly Glu Glu	Gly
	395	400	405
Leu Leu Ser Arg	Leu Tyr Glu Glu Pro	Ala Pro Asp Arg Pro	Pro
	410	415	420
Gly Glu Asn Glu	Thr Tyr Leu Met Gln	Phe Met Glu Glu Trp	Gly
	425	430	435
Leu Tyr Val Gln	Met Glu Asn		
	440		

<210> 105


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<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

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<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctgggtgt ttgcctaaac ctgcaaacat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cggacgcgtg ggcggacgcg tgggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgcat ggggctcggg ttgaggggct ggggacgtcc 100
tctgtgact gtggccaccg cctgatgtct gccctgaag cccccgcag 150
gtcctcgggg ggcccagatc atcggggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gccttcggg ggccaacatc actcggagg 250
cttctctgtg cgagcccgct ggggtggtctc gggcggccac tgcttcagcc 300
acagagacct ccgcactggc ctggtggtgc tgggcgcca cgtcctgagt 350
actcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400
cccagactac cccccatga ccacgccaa cgacatctgc ctgctcggc 450
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gggagaaggg ccaggccccc cacagcggg acacggtgcc ggggtgctgg 550
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ccaaggtccg agtgctggac ccggacgtct gcaacagctc ctggaaggcg 650
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ctcacggcct cgtttctctc tcgggcctct ggtgcggcga cccaagacc 800
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cccaggaga agccgcctga gccacaacct tcgggcatgc aaatgagatg 950
gccgtccagg gcctggaatg ttccgtggct gggcccccag ggaagcctga 1000
tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaagggc agaagcaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val	1	5	10	15
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp	20	25	30	
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg	35	40	45	
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly	50	55	60	
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys	65	70	75	
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala	80	85	90	
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile	95	100	105	
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala	110	115	120	
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly	125	130	135	
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro	140	145	150	
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val	155	160	165	
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val	170	175	180	
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His	185	190	195	
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg	200	205	210	
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg	215	220	225	
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly	230	235	240	
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val	245	250	255	

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccga ggcggctggt gtgcagcaag ctccgcgcgc actccggagc 50
ctgcgcgct gacgcctgtc cccggcccgc catgagccgc tacctgctgc 100
cgctgtcggc gctgggcacg gtagcaggcg ccgcccgtgt gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacaggcat cggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagacc ccaatcacca 350
 tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400
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 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagt 1450
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 ctgtctccca tgatggtgtg gtacagcgag ctgtgtctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccaggttc aggcctctgca cggcatggag 1700
 tggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttctca tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgcgtggca tgtggtcctg ggcgcggct ggcggcgtg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 ggcgcacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
 agcgcggct gctggggtg ctgaggcggg acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcatga 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcatct actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggaatggtat gagaaggtgg agcaagacct 400
 tccagccttt gaggacctg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
 agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagcttc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta ttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag ccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cacagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagcccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000
 ttccaacgcc tacctgtctc tccagcccat ccggaaggag gtcattccac 1050
 tggagcccta cattgtcttc taccatgact tcgtcagtga ctgagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac caaaactcgg tgacctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac ttgaccatg 1350
 ctactgcacc aagcagcccc ctctacagaa tgaagtccag aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggt gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag ccaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaaaggagg gggagtgga 1900
 ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggg 2050
 tagcctgact cccagaactt taagactttc tccccactgc cttctgtctc 2100
 agcccaagca gggagtgctc ccctcccaga agcatatccc agatgagtg 2150

tacattatat aaggattttt ttttaagttga aaacaacttt cttttctttt 2200
 tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 118
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
 1 5 10 15
 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Arg Gly Asp Thr
 20 25 30
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
 35 40 45
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
 50 55 60
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
 65 70 75
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
 80 85 90
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
 95 100 105
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
 110 115 120
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
 125 130 135
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
 140 145 150
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
 155 160 165
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
 170 175 180
 Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
 185 190 195
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Ala Val Ser Leu
 200 205 210
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
 215 220 225
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
 230 235 240

Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser	Val Glu Ala Gly Gly	Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser	Val Pro Val Val Arg	Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His	Arg Ser Gly Glu Gly	Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro	Val Leu Val Gly Asp	Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu	Tyr Gly Gln Glu Phe	Arg Arg Pro Cys Ser Ser			

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gaccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagataggga gtctgggttt aagttcctgc tccatctcag gagccctgc 50
tccccacctt aggaagccac cagactccac ggtgtggggc caatcagggtg 100
gaatcgccc ttgcagggtg ggccaagagc gctggctgag ggaccagacc 150
ggagagcccc ggagccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgtttct cctacctctg 250
 gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
 ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatectcct 400
 gggcgctcgc atgttcatgg tctccttcat tgggtgtctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550
 gaccattgac ttcttgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaagtgc 650
 aagtgtctgt gcggggaggga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gccctgggac ccttgacctg tggggtgccc tacacctgtc 750
 gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaaat 800
 atcgacaagg agcgtttcag tgtgcaggat gtcactctac tgcggggctg 850
 caccacgccc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcatcctcct gggcatcctg ctccccaggt tcctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccg gtgccaaagg cagcgtggag gcggcaggca 1050
 cggatgtctg cttgtgttac cccaattagg gccagcctg ccatggcgagc 1100
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
 ggacagggct gcggccctc tgcccacact cagtactgac caaagccagg 1200
 gctgtgtgtg cctgtgtgta ggtcccaagg cctctgcctc cccagggagc 1250
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 gtgccacct ggggcctggg gaacaaggcc ctcttctc caggcctggg 1350
 ctacagggga gggagagcct gaggtctcgc tcagggccca ttcatctct 1400
 ggcagtgcct tggcgggtgt attcaaggca gttttgtagc acctgtaatt 1450
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
 ctcttctcag cctccaggt gccttgagcc ctcttgcaag ggcggctgct 1600
 tccttgagcc tagtttttt ttacgtgatt ttgttaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggat ttccccgcac 1700
 gtcttattct tgcccttccc ccaaccagtt tggtaataca acaataaaaa 1750
 catgttttgt tttgttttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe	1	5	10	15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly	170	175	180	
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn	185	190	195	
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val	200	205	210	
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile	215	220	225	
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly				

	230		235		240
Ile	Leu	Leu	Pro	Gln	Phe
	245			Leu	Gly
			Val	Leu	Leu
			Thr	Leu	Tyr
				250	255

Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270

Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275										285

Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn
				290				


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<210> 124
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 124
atcatctatt ccaccgtgtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 125
gacagagtgc tccatgatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 126
cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
<211> 1636
<212> DNA
<213> Homo sapiens

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<400> 127
 gaggagcggg ccgaggactc cagcgtgcc aggtctggca tctgcactt 50
 gctgcctct gacacctggg aagatggcgg gccctggag cttaccctt 100
 ctctgtggtt tgctggcagc caccttgatc caagccacc tcagtccac 150
 tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
 agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
 agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
 ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta 350
 acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
 gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450
 gaccatcgtg gagtccaca tgacgactga ggcccaagcc accatccgca 500
 tggacaccag tgcaagtggc cccaccgcgc tggctctcag tgactgtgcc 550
 accagccatg ggagcctcgc catccaactg ctgtataagc tctccttctc 600
 ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650
 ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
 ggcatgtatg cagacctcct gcagctgggt aagggtccca ttccctcag 750
 cattgaccgt ctggagtttg accttctgta tctgccatc aagggtgaca 800
 ccattcagct ctacctggg gccaaagttgt tgactcaca gggaaagggt 850
 accaagtggt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
 caacatcccg ttcagcctca tcgtgagtca ggacgtgggt aaagctcgag 950
 tggctgctgt gctctctcca gaagaattca tggctcgtt ggactctgtg 1000
 cttctcgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050
 aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
 aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150
 ctgatcgtgc tggaaagtgt tccctccagt gaagccctcc gccctttgtt 1200
 caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggt 1250
 accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
 cactgagatc atccactcca tctgtctgcc gaaccagaat ggcaaattaa 1400
 gatctggggg cccagtgta ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
 gaaacccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
1				5					10					15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
				20					25					30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
				35					40					45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50					55					60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65					70					75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80					85					90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95					100					105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110					115					120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125					130					135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140					145					150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155					160					165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170					175					180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185					190					195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200					205					210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215					220					225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480
 Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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 ctaacaaaag acctgtaata agaataatg gagacaagtt ccgtcgccct 200
 gtgaaagccc caccgagaaa ttaactcgtt atcgtcatgt tcaactgctc 250
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
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 ccaaacgggg tgatacatat gaggttacagg tgcggggttt ttcagctgag 500
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 aataaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
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 ctttctgatg agttaaaag gtcccagaga tatatagaca ctggagtact 1050
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 gtatathtt gattacctct ttttttcaag tgatttaaat agttaatcat 1150
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 aactactact ttgttttagt tagaacaag ctcaaaacta ctttagttaa 1350
 cttggtcatc tgattttata ttgccttata caaagatggg gaaagtaagt 1400
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 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaac 1950
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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
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Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20					25					30
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35					40					45
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50					55					60
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65					70					75
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80					85					90
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
				95					100					105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
 110 115 120
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
 125 130 135
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
 140 145 150
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
 155 160 165
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 170 175 180
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
 185 190 195
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
 200 205 210
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 215 220 225
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
 245 250 255
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
 260 265 270
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
 275 280 285
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
 290 295 300
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
 305 310 315
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
 320 325 330
 Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 aggttaacat ttcatccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga ctctctttct gaatgcctac acaaacctctc 350
 caatttgttg cccatcacgc gcagcaatgt ggagtggcct cttcaactcac 400
 ttaacagaat cttggaataa ttttaagggt ctatagccaa attatacaac 450
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 aactggacta tacttcagga catcactcca tttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt ctactcaga caagaaggca ggcccatggt 600
 taatcttacc cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
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 actgaaccat ttgttattta ctggggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaaat cccaaagtgg 850
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 ttggcccttc atcaattaga tcttcttcag aaaactattg tcataatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
 gcatgtacga ggctagtaca catgtccgc ttttgatgat gggaccagga 1150
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 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagtg 1250
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 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350
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 cctattcgga tgggtcatca atattgcctc aactctttga tcttctctcg 1450
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 tcttttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

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 acctgtaat ccaggacttt gggaggctga ggaagcaga tcacaaggctc 1900
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 atgttccttt aaataataga gaataataaa tattgtaata atatgtatca 2350
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<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
				20					25				30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg
				35					40				45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile
				50					55				60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr
				65					70				75	

Asn Ser Pro Ile	Cys Cys Pro Ser Arg	Ala Ala Met Trp Ser Gly
	80	85 90
Leu Phe Thr His	Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu	
	95	100 105
Asp Pro Asn Tyr	Thr Thr Trp Met Asp Val Met Glu Arg His Gly	
	110	115 120
Tyr Arg Thr Gln	Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His	
	125	130 135
His Ser Ile Ser	Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala	
	140	145 150
Phe Leu Leu Arg	Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg	
	155	160 165
Asn Arg Thr Lys	Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr	
	170	175 180
Asp Lys Ala Val	Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr	
	185	190 195
Glu Pro Phe Val	Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr	
	200	205 210
Pro Ser Pro Ser	Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His	
	215	220 225
Thr Ser Leu Tyr	Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys	
	230	235 240
Ile Pro Lys Trp	Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr	
	245	250 255
Tyr Ser Ser Tyr	Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	
	260	265 270
Glu Ile Lys Asn	Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	
	275	280 285
Thr Asp Ala Met	Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	
	290	295 300
Asp Leu Leu Gln	Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	
	305	310 315
Glu Leu Ala Met	Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	
	320	325 330
Glu Ala Ser Ala	His Val Pro Leu Leu Met Met Gly Pro Gly Ile	
	335	340 345
Lys Ala Gly Leu	Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	
	350	355 360
Tyr Pro Thr Met	Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn	

	365		370		375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu Ser	Glu Thr Phe Lys			
	380	385			390
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser			
	395	400			405
Glu Phe His Gly	Cys Asn Val Asn Ala Ser	Thr Tyr Met Leu Arg			
	410	415			420
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser			
	425	430			435
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr			
	440	445			450
Asn Val Ala Val	Lys Phe Pro Glu Ile Thr	Tyr Ser Leu Asp Gln			
	455	460			465
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val			
	470	475			480
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile			
	485	490			495
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln			
	500	505			510
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln			
	515	520			525
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val			
	530	535			

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 ctacatccta ggccttctgg ggccttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggtggaa tgtgccacac acagcacagg 300
 catcaccagc tgtgacatct atagaccctc tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctcg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
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 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

	50		55		60
Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro	Ala		
65		70		75	
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser	Ala Ile		
80		85		90	
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg	Cys Thr		
95		100		105	
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala	Val Ala		
110		115		120	
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe	Ile Pro		
125		130		135	
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr	Ser Pro		
140		145		150	
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala	Leu Tyr		
155		160		165	
Leu Gly Ile Ile Ser	Ser Leu Phe Ser	Leu Ile Ala Gly	Ile Ile		
170		175		180	
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn	Tyr Tyr		
185		190		195	
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser	Pro Arg		
200		205		210	
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser	Tyr Ser		
215		220		225	
Leu Thr Gly Tyr Val					
230					

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcacgc tcccgtggc tcagaacct ggctgtgcca gccggcacc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tcctgagcg agaccgcga atgtgtgcc cctgcacct 250
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 gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccaetc 350

atctcccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
			20						25					30
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
			35						40					45
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
			50						55					60
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
			65						70					75
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
			80						85					90
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
			95						100					105
Cys	Arg	Ser	Val	Ser										
				110										

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgcctctcgc 200
 tctcttctgc gctgcgtccc taggtccggt ggcagccttc aaggtcgcga 250
 cgccgtatcc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaagg cagcatgtga ccttctacaa 350
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 gggaggtga gtggagagg gcacctgccc cccgccctcc ccaccccta 1900
 ctccactgc tcagcgggg ccattgcaag ggtgccacac aatgtcttgt 1950
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<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
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 20 25 30
 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

	140		145		150
Ile Arg His His Ser Glu His Arg Val His Gly Ala Met Glu	155		160		165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val	170		175		180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala	185		190		195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu	200		205		210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg	215		220		225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile	230		235		240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro	245		250		255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln	260		265		270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro	275		280		285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp	290		295		300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile	305		310		

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 ccttctccga ccccgctcta gcagcagacc tcttggggc tgtgggtga 200
 tctgtggccc ctgtgctcc gtgtctttt cgtctccct cctccgact 250
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 agatactccc ccgagagag ctggcacc cttctggagc cacaaggct 450

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<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

	290		295		300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro	305		310		315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg	320		325		330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser	335		340		345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala	350		355		360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu	365		370		375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His	380		385		390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala	395		400		405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro	410		415		420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala	425		430		435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys	440		445		450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200
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gaaatccac aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
			20						25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
			35						40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
			65						70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
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<210> 148
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 148

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Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
				20					25					30
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu	Lys		
	245		250		255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu	Asp		
	260		265		270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg	Lys		
	275		280		285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro	Lys		
	290		295		300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala	Pro		
	305		310		315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser	Val		
	320		325		330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu	Val		
	335		340		345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg	Asp		
	350		355		360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp	His		
	365		370		375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe	Thr		
	380		385		390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro	Thr		
	395		400		405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser	Phe		
	410		415		420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys	Arg		
	425		430		435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr	Asn		
	440		445		450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln	Glu		
	455		460		465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro	Glu		
	470		475		480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe	Leu		
	485		490		495
Pro Arg Gly Glu	Met				
	500				

<210> 149

<211> 24

<212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 149
 gcgtggtcca cctctacag gacg 24

 <210> 150
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 150
 ggaactgacc cagtgtgac acc 23

 <210> 151
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 151
 gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

 <210> 152
 <211> 2294
 <212> DNA
 <213> Homo sapiens

 <400> 152
 gcgatggtgc gcccggtggc ggtggcggcg gcggttgcgg aggccttcctt 50
 ggtcggattg caacgagag aagatgactg accaaccgac tggctgaatg 100
 aatgaatggc ggagccgagc gcgccatgag gaggctgcgg agcctggggc 150
 gcctgcgcct gttgtgctgc gccgccgccg ccgcccgcgt cgcctcagcc 200
 gcctcggcgg ggaatgtcac cggtagggcg gggccggcg ggcagtgga 250
 cgcgtcgccg gggccgggt tggggggcga gccagccac cccttcctta 300
 gggcgacggc tcccacggc caggccccga ggaccgggc cccgcgcgcc 350
 accgtccacc gaccctggc tgcgacttct ccagccagc cccggagac 400

caccctctt tggcgactg ctggaccctc ttcaccacc ttccaggcgc 450
 cgctcgccc ctgcccgacc acccctccg cgcggaacg cacttcgacc 500
 acctctcagg cgccgaccag acccgcccg accaccctt cgacgaccac 550
 tggcccgcg cgaccacc ctgtagcgac caccgtaccg gcgcccacga 600
 ctccccgac ccgaccccc gatctccca gcagcagcaa cagcagcgtc 650
 ctccccccc cactgccac cgaggccccc tcttcgcctc ctccagagta 700
 tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
 agaccacagg gcagtgtgag tgcggccag gttatcaggg gcttactagt 800
 gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
 gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
 aagcaacaga ggggtgaact gaagtttatt ttatttttagc aagggaataa 950
 aaaaggctgc tactctcaag gaccatactg gtttaacaa aggaggatga 1000
 gggtcataga ttacaaaa attttatata cttttattct cttactttat 1050
 atgttatatt taatgtcagg atttaaaac atctaattta ctgatttagt 1100
 tcttcaaaag cactagagtc gccaatttt ctctgggata atttctgtaa 1150
 atttcatggg aaaaaattat tgaagaataa atctgcttct tgggaaggct 1200
 ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
 atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300
 taatcaaaa tctacattg ttcttttga catctaaagc ttaacctggg 1350
 ggtaccctaa tttatttaac tagtggtgaag tagactggtt ttactctatt 1400
 taccagtaca ttttgagac caaaagtaga ttaagcagga attatcttta 1450
 aactattatg ttatttgag gtaatttaat ctagtgaat aatgtactgt 1500
 tatctaagca ttgacctgt actgactga aagtaattat tctttgacct 1550
 tatgtgaggc acttgcttt ttgtggacc caagtcaaaa aactgaagag 1600
 acagtattaa ataatgaaa aaataatgac aggttatact cagtgaacc 1650
 tgggtataac coaagatctg ctgccactta cgagctgtgt tccctgggca 1700
 agtaatttcc ttctactgag cttgtttctt ctcaagggtg ttgtgaagat 1750
 taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
 ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcctt atacttttagc 1900
 actaaatatt ttaaatgcct tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctacagcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100
 ctactaaaaa tacaacaaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro

	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly Tyr	Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu				
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro				
	245	250			255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tgggtggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggtttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcctt ggtctcggtg cccagggccc aggcctgtg gtgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtgccctc 150
 cggggaag ggctttgcc tggagaagga catgaagaac gtcgtggggg 200
 tgggtgtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgga ccagagtgtc atggacctga taaagcgaag 300
 ctccgatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcc tcatcttcac tcagctggag 400
 ttctggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggcatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctgtgc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
 gggctctgtg acctcgcca gtgtccacc acctcgctca gcggtcccg 650
 gggccagca ccagctcaga ataaagcat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
 95 100 105
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
 110 115 120
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
 125 130 135
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
 140 145 150
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
 155 160

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgtgtgt 50
 gctgtgtgtg cccctgtctt gggggaggga gagggcggaa ggacagacaa 100
 gtaaacgtgt gacgatgcag agttccgtga cgtgacgga aggcctgtgt 150
 gtccatgtgc cctgtctcct ctcctacccc tcgcatggct ggatttaccc 200
 tggcccagta gttcatggct actgggtccg ggaaggggcc aatacagacc 250
 aggatgtctc agtggccaca aacaacccag ctcgggcagt gtggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctctt 450
 gtgaattgta cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaattcgac ctgctctgtg cctcgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggatagggac ctcctgtgcc 600
 cccctggacc cctccaccac ccgctcctcg gtgtcacccc tcatccaca 650
 gccccaggac catggcacca gctcacctg tcaggtgacc ttcctgggg 700
 ccagcgtgac cagcaacaag accgtccatc tcaacgtgtc ctaccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
 tggctctgtc agttgatgca gttgacgca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100
 tggagccaca gccctggtct tcctgtcctt ctgcgtcacc ttctgttag 1150
 tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250
 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttcagca tggatgaagc ttgggactcg cggggacagg aggccaactga 1400
 caccgagtag tcggagatca agatccacag atgagaaact gcagagactc 1450
 acctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttct agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctg atccacactg tgccctccct tttattttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1				5					10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

	110		115		120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	125		130		135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140		145		150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155		160		165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170		175		180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185		190		195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200		205		210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215		220		225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230		235		240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245		250		255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260		265		270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275		280		285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290		295		300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305		310		315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320		325		330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335		340		345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350		355		360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365		370		375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380		385		390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395		400		405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgccagtgacctgcccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaagt gtccccagt 200
 aaggtgacag ccctgggagg tgggaagtgt gaagccacgt tcaccttcac 250
 gaggaggagat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgccca ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagc caagggagctc 500
 tcggaggagg acattttcac gccctgcag acgggaaagt cgttcccgca 550
 acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttccct 650
 gctccccccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

	20		25		30
Val Lys Ala Met	Val Val Asp Lys Asp	Phe Pro Glu Asp Arg Arg			
	35	40		45	
Pro Arg Lys Val	Ser Pro Val Lys Val	Thr Ala Leu Gly Gly Gly			
	50	55		60	
Lys Leu Glu Ala	Thr Phe Thr Phe Met	Arg Glu Asp Arg Cys Ile			
	65	70		75	
Gln Lys Lys Ile	Leu Met Arg Lys Thr	Glu Glu Pro Gly Lys Tyr			
	80	85		90	
Ser Ala Tyr Gly	Gly Arg Lys Leu Met	Tyr Leu Gln Glu Leu Pro			
	95	100		105	
Arg Arg Asp His	Tyr Ile Phe Tyr Cys	Lys Asp Gln His His Gly			
	110	115		120	
Gly Leu Leu His	Met Gly Lys Leu Val	Gly Arg Asn Ser Asp Thr			
	125	130		135	
Asn Arg Glu Ala	Leu Glu Glu Phe Lys	Lys Leu Val Gln Arg Lys			
	140	145		150	
Gly Leu Ser Glu	Glu Asp Ile Phe Thr	Pro Leu Gln Thr Gly Ser			
	155	160		165	
Cys Val Pro Glu	His				
	170				

<210> 163

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.

 <400> 165
 gtcctccgga aagtccttat c 21

 <210> 166
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 166
 gcctagtggt cggaacgca gcttc 25

 <210> 167
 <211> 50
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

 <400> 167
 cagggaacctg gtacgtgaag gccatgggtg tcgataagga cttccggag 50

 <210> 168
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 168
 ctgtccttca ccctggagga ggaggatatc acagggaacct ggtac 45

 <210> 169
 <211> 1204
 <212> DNA
 <213> Homo sapiens

 <400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
 cagaggtctc acagcagcca aggaacctgg ggcccgtccc tccccctcc 100
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacaggggctt 150
 gtatggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
 cgacgctcat cgccccaga ttgctcctga cagcagccca ctgcctcaag 300
 ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
 ctgtgagcag acccggaacag ccaactgagtc ctccccccac cccggcttca 400
 acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450
 atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
 ctcaagctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaaac 650
 cacagacacc atgggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccagggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctctt ggggccagga tccgtgtgcg atcaccggaa agcctggtgt 800
 ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcaccctc catttccact 900
 tgggtgtttg ttctgttca ctctgttaat aagaaccctc aagccaagac 950
 cctctacgaa cattcttttg gcctcctgga ctacaggaga tgctgtcact 1000
 taataataca cctgggggtc gaaatcagtg agacctggat tcaaatcttg 1050
 ccttgaaata ttgtgactct gggaaatgaca acacctggtt tgttctctgt 1100
 tgtatcccca gccccaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatattgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
 1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
 20 25 30
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
 35 40 45
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50 55 60
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 65 70 75
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
 80 85 90
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 95 100 105
 Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
 110 115 120
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 125 130 135
 Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
 140 145 150
 Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
 155 160 165
 Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
 170 175 180
 Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
 185 190 195
 Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
 200 205 210
 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
 215 220 225
 Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
 230 235 240
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
 245 250

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
 ggctgcgga ctggaagtca tcggg 25

 <210> 172
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 172
 ctccaggcca tgaggattct gcag 24

 <210> 173
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 173
 cctctgggtct gtaaccag 18

 <210> 174
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 174
 tctgtgatgt tgccggggta ggcg 24

 <210> 175
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 175
 cgtgtagaca ccaggcttct ggggtg 25

 <210> 176
 <211> 18
 <212> DNA

<213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.
 <400> 176
 cccttgatga tcctggtc 18
 <210> 177
 <211> 50
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.
 <400> 177
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 50
 <210> 178
 <211> 43
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.
 <400> 178
 gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43
 <210> 179
 <211> 907
 <212> DNA
 <213> Homo sapiens
 <400> 179
 gagcagtggt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
 gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100
 aagaaagagg agagcacoga agaagtgaat atagaagttt tgcacgtccc 150
 agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccattt 200
 atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
 caaaatgaag gccaccccaa atggtttgtt ctgtgtgttg ggcaagtc 300
 aaaaggcta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
 aagtagttat acccccttca tttgcatacg gaaaggaag ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgacccaaa ggaccacgga gcattgagac atttaacaa atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta ctggcaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatac aggatgcagt 600
 tttagaagat atttttaaga agaattgacca tgatggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 attctactt ttttttttta gctatttact gtacttttatg tataaaacaa 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850
 ttgc aaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met	Pro	Lys	Thr	Met	His	Phe	Leu	Phe	Arg	Phe	Ile	Val	Phe	Phe
1				5					10					15
Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu
				20					25					30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn
				35					40					45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr
				50					55					60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg
				65					70					75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly
				80					85					90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro
				95					100					105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly
				110					115					120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu
				125					130					135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser
				140					145					150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	
				155					160					165	
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	
				170					175					180	
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	
				185					190					195	
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	
				200					205					210	
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				
				215					220						

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 184
 gatgtctgcc accccaag 18

 <210> 185
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

 <400> 185
 gcattctgat atgacttgct acgtggc 27

 <210> 186
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 186
 tacaagaggg aagaggagtt gcac 24

 <210> 187
 <211> 52
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

 <400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

 cc 52

 <210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

 <400> 188
 cagaaatgca gggaccattg cttcttcag gcctctgctt tctgctgagc 50

 cttcttgag ctgtgactca gaaaaccaa acttctgtg ctaagtgtcc 100

cccaaatgct tctgtgtca ataacaetca ctgcacctgc aacctggat 150
 atactttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaac ccggtgtcta ctaaaaatac aaaaalcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggcctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgttcc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10					15

Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20					25					30

Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
			35						40					45

Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
			50						55					60

Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu
			65						70				

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 192
 cctgtgctaa gtgccccca aatgcttctt gtgtcaataa cactcactgc 50

<210> 193
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 193
 caagcaggtc atcccccttg tgaccttcaa agagaagcag agagggcaga 50
 ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
 gactttggaa gtgaccacc atggggctca gcatctttt gctcctgtgt 150
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
 gtgtgggct aactcacagc cgtggcaggt gggctgttt gagggcacca 250
 gctcgcgtg cgggggtgtc cttattgacc acagtggggt cctcacagcg 300
 gctcactgca gcgcagcag gtactgggtg cgcctggggg aacacagcct 350
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
 ctgctcgggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500
 gccctgccc aatgactgtg caaccgctgg caccgagtgc cagctctcag 550
 gctggggcat caccaaccac ccacggaacc cattccggga tctgtctcag 600
 tgcttcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
 cgggagaatc acgagcaaca tgggtgtgtc aggcggcgct ccggggcagg 700
 atgcctgcca gggtgattct gggggccccc tgggtgtgtg gggagtcctt 750
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900
 ctgggtacc cctctggccc tcagagacc aatatctct ccatcattc 950
 ccctagctcc actctgttg gcttggaac ttcttggaac tttactcct 1000
 gccagccctt ctaagacca cgagcgggt gagagaagt tgcaatagtc 1050
 tgaataaat ataatgaag gaggggcaaa aaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgccct gtgcctctctc 50
 ctgcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgcttc 150
 ggcttgctca aagcccgga ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagccctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggt acaggagggg 400
 tcagtacac tatatctac cgagacttg tgaacatgat gctggggaaa 450
 cggtcggtg tctcaagtt agtcatgatg ttgaaggaa aagccaacga 500
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg accccgcctg gactccccag ccttccacc ccatacctcc 600
 ctcccgatct tgcgtccctt cttgacacac tgtgatctct ctctctctca 650
 tttgtttggt cattgagggt ttgtttgtgt ttcatcaat gtctttgtaa 700
 agcacaatt atctgcctta aagggctctt gggtcggga atcctgagcc 750
 ttgggtcccc tccctctctt cttccctcct tcccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850
 cttccagcct gtgttccct cacttgagg aaccagcact ctccatcctt 900
 tcagaaagtc tcaagccaa gttcaggctc actgacctgg ctctgacgag 950
 gacccagc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttccttg acagtgccat ggttccagt ctctggtgtc 1050

acccaggaca cagccactcg gggcccccgt gcccagctg atccccactc 1100
 attccacacc tcttctcatc ctcaagtatg tgaaggtggg aaggaaagga 1150
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 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
 tgggggttgg ggggaaaggt cagctcagt ctgtccacc ttttagggag 1350
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgctgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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cagcctctct caggagcggg gccctgcaca ccattggccc cgggtgggca 100
ggggtcggcg ccgccgtgcg cggccgcctg cgcgtggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagcgcgtcg ctgcccacc aagtgtacct 200
gtcgcgtgca cagcgtggac tgccaacggc tgggcctccg cgcggttcct 250
cggggcatcc cccgcaacgc tgagcgctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcattctga agacaaccag gtcagcgta tcgagagagg cgccttccag 400
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttcagaaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagattccag gggatcccg ggaaggcgtt ccgcggcacc 550
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650
acaacaacat cagtcgcacc ctggtcacca gcttcaacca catgccgaag 700
atccgaactc tgcgcctcca ctccaaccac ctctactgag actgccacct 750
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800
cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggaatgt 850
cagaagaagg agtacgtgtg cccagccccc cactcgagc ccccatcctg 900
caatgccaac tccatctctt gcccttcgcc ctgcacgtgc agcaataaca 950
tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000
gagggcatcg tcgaaatagc cctagaacag aactccatca aagccatccc 1050
tgcaggagcc ttcacccagt acaagaaact gaagcgaata gacatcagca 1100
agaatcagat atcgatatt gctccagatg ccttccaggg cctgaaatca 1150
ctcacatcgc tggctcgtga tgggaacaag atcaccgaga ttccaagg 1200
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agatcaactg cctcggggtg aacacgtttc aggacctgca gaacctcaac 1300
ttgctctccc tgtatgacaa caagctgcag accatcagca agggctctt 1350
cgccctctg cagtcacatc agaacctcca cttagccaa aacctattg 1400
tgtgcgactg ccacttgaag tggtggcgg actacctcca ggacaacccc 1450

atcgagacaa gcggggcccg ctgcagcagc ccgcgccgac tcgccaacaa 1500
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 attaccgcag caggttcagc agcgagtgtc tcatggacct cgtgtgcccc 1600
 gagaagtgtc gctgtgaggg cagcattgtg gactgctcca accagaagct 1650
 ggtcgcgcatc ccaagccacc tccctgaata tgcaccgac ctgcgactga 1700
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 agagggagct ttcgatggag cagccagcgt gcaggagctg atgctgacag 1850
 ggaaccagct ggagaccgtg cacgggcgcg tgttccgtgg cctcagtgcc 1900
 ctcaaaacct tgatgctgag gagttaactg atcagctgtg tgaagtaatga 1950
 cacctttgcc ggcttgagtt cggtgagact gctgtccctc tatgacaatc 2000
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 accataaacc tctgtgctca ccccttcaac tgcaactgcc acctggcctg 2100
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gtgatccgcc gccagaaagg ttatgcata tgtgccacag cctccaaggt 4500
gcccatcatg gaatgtcgtg ggggctgtg gccccagtgc tgccagccca 4550
ccgcagcaaa gcgcggaaa tacgtcttcc agtgcacgga cggtcctcg 4600
tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttc 4650
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gttgggacag ccattgtgga cccctgtgtg attcagcatg aaggaaatga 4750
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aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
1 5 10 15
Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
20 25 30
Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

	455		460		465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470	475	480		
Lys Lys Phe Arg	Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe			
	485	490	495		
Ser Ser Glu Cys	Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg			
	500	505	510		
Cys Glu Gly Thr	Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg			
	515	520	525		
Ile Pro Ser His	Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn			
	530	535	540		
Asp Asn Glu Val	Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys			
	545	550	555		
Leu Pro Asn Leu	Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys			
	560	565	570		
Glu Val Arg Glu	Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu			
	575	580	585		
Leu Met Leu Thr	Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val			
	590	595	600		
Phe Arg Gly Leu	Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn			
	605	610	615		
Leu Ile Ser Cys	Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser			
	620	625	630		
Val Arg Leu Leu	Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr			
	635	640	645		
Pro Gly Ala Phe	Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu			
	650	655	660		
Leu Ser Asn Pro	Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly			
	665	670	675		
Lys Trp Leu Arg	Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys			
	680	685	690		
Gln Lys Pro Phe	Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala			
	695	700	705		
Ile Gln Asp Phe	Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln			
	710	715	720		
Leu Ser Pro Arg	Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val			
	725	730	735		
Val Arg Cys Ser	Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met			
	740	745	750		

Pro Lys Asp Val Thr	Glu Leu Tyr Leu	Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg Glu	Leu Ser Ala Leu	Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn Asn	Ser Ile Ser Met	Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser His	Leu Ser Thr Leu	Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile Pro	Val His Ala Phe	Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr Leu	His Gly Asn Asp	Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn Asp	Leu Thr Ser Leu	Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu His	Cys Asp Cys Ser	Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala Gly	Tyr Lys Glu Pro	Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro Met	Ala Asp Arg Leu	Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln Cys	Lys Gly Pro Val	Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala Cys	Leu Ser Ser Pro	Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp Pro	Val Glu Leu Tyr	Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly Lys	Asp Cys Thr Val	Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys Gln	His Gly Gly Thr	Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly Phe	Ser Cys Ser Cys	Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu Ile	Asn Pro Asp Asp	Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala Thr	Cys Val Asp Gly	Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro Asn	Tyr Thr Gly Glu	Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val Pro	Glu Leu Asn Leu	Cys Gln His Glu Ala Lys			

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Glu Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
 1505 1510 1515
 Glu Cys Gly Cys Leu Ala Cys Ser
 1520

<210> 199
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 199
 atggagattc ctgccaaactt gccg 24

<210> 200
 <211> 24
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgccat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccctcg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtcctaaa 200
atctacactc gttgcaaaact ggcaaaaaata ttctcgaggg ctggcctgga 250
caattactcg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgccg gaaaaattgt taaagagaca 500
caaggaaatga actattggca aggctggaag aaacattgtg agggcagaga 550
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gagggaataa taagctatac tttaagaaa ataaatattt ccatttaaat 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
 ctcattggct gcctggcac aggc 24

 <210> 206
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 206
 ccagtcggac aggtctctcc cctc 24

 <210> 207
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 207
 tcagtgacca aggctgagca ggcg 24

 <210> 208
 <211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 208
 ctacactcgt tgcaaacctgg caaaaatatt ctcgagggct ggcctgg 47

 <210> 209
 <211> 1648
 <212> DNA
 <213> Homo sapiens

 <400> 209
 caggccattt gcacccact gtccttgtgt tcggagccag gccacaccgt 50

 cctcagcagt gtcattgttt aaaaacgcca agctgaatat atcatgcccc 100

 tattaaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150

 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200

 gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaa cgactatata gggccccaat tgactggata 300
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaatgtca ccagctttga ctcagttggt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tccctgtgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcaactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600
 catctgatcg tggcagggtg ttatgacgag agagtccctg agaatgtgga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
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 tgctctctctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
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 ataagagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcactgtcat ctgttaggga atttttgttt gtctgtctt tgccctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaagggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210
 <211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
1				5					10					15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro	Asp	Pro	Val	His	Phe	Ser	Glu	Ala	Ile	Glu	Lys	Phe	Ile	Arg	
				275					280					285	
Glu	Pro	Ser	Leu	Lys	Ala	Thr	Met	Gly	Leu	Ala	Gly	Arg	Ala	Arg	
				290					295					300	
Val	Lys	Glu	Lys	Phe	Ser	Pro	Glu	Ala	Phe	Thr	Glu	Gln	Leu	Tyr	
				305					310					315	
Arg	Tyr	Val	Thr	Lys	Leu	Leu	Val								
				320											

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
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 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
 tttgcatgag ttcttggtta atttgcatga gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctctggttga gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg cctctcctct aaagctttca gaagaattat tagataaatg 500
 gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctggt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcatctg ctccagaag aatcatggca cagtttggtc 650
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ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
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 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
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 ttaa 1554

<210> 212

<211> 462

<212> PRM

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu	1	5	10	15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	20	25	30	
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	35	40	45	
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	50	55	60	
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	65	70	75	
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	80	85	90	
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	95	100	105	
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Ser	Val	Ser	Glu	Asn		110	115	120	
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	125	130	135	
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu				

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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 tcagggttg tgccctctcg ctctcgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gctgcctgc 200
 ctctcacgtt cacccccag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtcaccct gggcctctt gcagtggagc tggccggtt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggtcactg tagtgcatcc gtggcctgt ccttcttcat attcgagcgt 400
 tgggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aaccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttcccctcg aaactgcttc tgctggagga tatgtgttg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttag taacattaag acttatatac agtttttagg gacaataaa 750
 aaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
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 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

<213> Homo sapiens

<400> 216

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 1           5           10           15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20           25           30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35           40           45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50           55           60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65           70           75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80           85           90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95           100          105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110          115          120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125          130          135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140          145          150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155          160          165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170          175          180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185          190          195
Pro
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<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtctcccggg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcgga 200
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gggggggccac atctcaccta agtccccgcc catggccaat tccactctcc 250
 tagggctgct gggcccgccct ggggaggett ggggcattct tgggcagccc 300
 cccaacgcc cgaaccacag cccccccccc tcagccaagg tgaagaaaa 350
 ctttgctgg ggcgacttct actccaacat caagacgggt gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcacgt 550
 aagccaaggc ctccaaaaat ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
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 cccatctgg tgaccgggg caggccacag aggccaggcc agggctgaa 850
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 aataaagctt gccccggggc a 1871

<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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tcacagatta ttgtgtgtg tctgtttcag tatatttga ttgggactct 1150
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 gaaaactcta aagttctgac ttcaatcaac ggttagtgtg ataactgcaa 1350
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 ccaagttata ttttctaaga agaagaatag atcataaatc tgacaaggaa 1650
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 ttcaaatatc ccataatctaa atttagtgca atatctgtgc tttgtatag 2000
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 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
 1 5 10

Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
 20 25 30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
 35 40 45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
 50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
 65 70 75
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
 140 145 150
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
 170 175 180
 Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
 185 190 195
 Phe Leu Val Phe Pro Leu
 200

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
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<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttgag tccg 24

<210> 223
 <211> 40

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<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgctgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tatcatcttc ctcatgcgcg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
tatccaagaa atgttccgat ttgcataatta taaactctta aaaaaagcca 300
gtgaagggtt gaagagtata aaccagggtg agacagcacc ctctatgcga 350
ctgctggcct atgtttctcg cttgggcctt ggaatcatga gtggagtatt 400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600
tggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccc cagactacat ctttagagga agcacaactg tgcctttttc 850
tgaaaatccc tttttctggt ggaattgaga aagaataaaa actatgcaga 900
ta 902

<210> 225
<211> 257
<212> PRT

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<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly
1				5					10					15
Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20					25					30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
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Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Gly
				50					55					60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65					70					75
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95					100					105
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
				110					115					120
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn
				125					130					135
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly
				140					145					150
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
				155					160					165
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly
				170					175					180
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190					195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205					210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220					225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235					240
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<211> 3939
 <212> DNA
 <213> Homo sapiens

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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25				30	

Lys Asp Ala Glu	Phe Glu Arg Thr Tyr	Val Asp Glu Val Asn Ser	
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Glu Leu Val Asn	Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn		
	50	55	60
Arg Thr Glu Gly	Val Arg Val Ser Val Asn Val Leu Asn Lys Gln		
	65	70	75
Lys Gly Ala Pro	Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val		
	80	85	90
Val Ser Phe Gln	Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg		
	95	100	105
Lys Tyr Leu Tyr	Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro		
	110	115	120
Thr Lys Asn Glu	Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser		
	125	130	135
Thr Leu Ser Pro	Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg		
	140	145	150
Met Asp Asp Phe	Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn		
	155	160	165
Thr Thr Ala Ala	Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu		
	170	175	180
Gly Val Asp Ser	Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe		
	185	190	195
Pro Cys Ser Val	Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr		
	200	205	210
Asp Leu Asp Asn	Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met		
	215	220	225
Thr Lys Lys Ala	Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser		
	230	235	240
Asn Ser Phe Tyr	Val Val Val Val Val Lys Thr Glu Asp Gln Ala		
	245	250	255
Cys Gly Gly Ser	Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro		
	260	265	270
Val Asp Gln Gly	His Arg Gln Lys Thr Leu Ser Val Leu Val Ser		
	275	280	285
Gln Ala Val Thr	Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys		
	290	295	300
Leu Gly Ile Phe	Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala		
	305	310	315
Cys Trp Glu Asn	Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala		

	320		325		330
Ile Asp Arg Ala	Cys Pro Glu Ser Gly His	Pro Arg Val Leu Ala			
	335	340			345
Asp Ser Phe Pro	Gly Ser Ser Pro Tyr Glu	Gly Tyr Asn Tyr Gly			
	350	355			360
Ser Phe Glu Asn	Val Ser Gly Ser Thr Asp	Gly Leu Val Asp Ser			
	365	370			375
Ala Gly Thr Gly	Asp Leu Ser Tyr Gly Tyr	Gln Gly Arg Ser Phe			
	380	385			390
Glu Pro Val Gly	Thr Arg Pro Arg Val Asp	Ser Met Ser Ser Val			
	395	400			405
Glu Glu Asp Asp	Tyr Asp Thr Leu Thr Asp	Ile Asp Ser Asp Lys			
	410	415			420
Asn Val Ile Arg	Thr Lys Gln Tyr Leu Tyr	Val Ala Asp Leu Ala			
	425	430			435
Arg Lys Asp Lys	Arg Val Leu Arg Lys Lys	Tyr Gln Ile Tyr Phe			
	440	445			450
Trp Asn Ile Ala	Thr Ile Ala Val Phe Tyr	Ala Leu Pro Val Val			
	455	460			465
Gln Leu Val Ile	Thr Tyr Gln Thr Val Val	Asn Val Thr Gly Asn			
	470	475			480
Gln Asp Ile Cys	Tyr Tyr Asn Phe Leu Cys	Ala His Pro Leu Gly			
	485	490			495
Asn Leu Ser Ala	Phe Asn Asn Ile Leu Ser	Asn Leu Gly Tyr Ile			
	500	505			510
Leu Leu Gly Leu	Leu Phe Leu Leu Ile Ile	Leu Gln Arg Glu Ile			
	515	520			525
Asn His Asn Arg	Ala Leu Leu Arg Asn Asp	Leu Cys Ala Leu Glu			
	530	535			540
Cys Gly Ile Pro	Lys His Phe Gly Leu Phe	Tyr Ala Met Gly Thr			
	545	550			555
Ala Leu Met Met	Glu Gly Leu Leu Ser Ala	Cys Tyr His Val Cys			
	560	565			570
Pro Asn Tyr Thr	Asn Phe Gln Phe Asp Thr	Ser Phe Met Tyr Met			
	575	580			585
Ile Ala Gly Leu	Cys Met Leu Lys Leu Tyr	Gln Lys Arg His Pro			
	590	595			600
Asp Ile Asn Ala	Ser Ala Tyr Ser Ala Tyr	Ala Cys Leu Ala Ile			
	605	610			615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
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Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
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Arg	Asp	Lys	Ile	Tyr	Val	Phe									
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 <211> 2848
 <212> DNA
 <213> Homo sapiens

<400> 228
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 <211> 807
 <212> PRT
 <213> Homo sapiens

<400> 229
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				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Val	Leu	Ala	Met		
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
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Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485					490					495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
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Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515					520					525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560					565					570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
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Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590					595					600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

	605		610		615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp		
	620	625	630		
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu		
	635	640	645		
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His		
	650	655	660		
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser		
	665	670	675		
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val		
	680	685	690		
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr		
	695	700	705		
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile		
	710	715	720		
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val		
	725	730	735		
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg		
	740	745	750		
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val		
	755	760	765		
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile		
	770	775	780		
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp		
	785	790	795		
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
	800	805			

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgccctaccg cgcagcccga agattcacta tggtagaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aacccactc cag 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagctctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
ccggggacat gaggtggata ctgttcattg ggcccttat tgggtccagc 50
atctgtggcc aagaaaaatt ttttggggac caagttttga ggattaatgt 100
cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttcttg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaaat ccttctctgag 250
atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccttgaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccgtt tggtggaatg caggcatcca 550
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ggaaaggggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850

cgccaattcg gaagtggagg tgaatcagtg gtagatttc atccaaaaac 900
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 cgacaagggt gcgaggcttg cggccaaagc tctggctctt gtgtcgggca 1050
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 aagaactggt tctgccagcc tgctcaattt tggctctgct gtttttgatg 1500
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 ctctgctccc tgggttcaag caattctcct gcctcagcct cttgagtagc 1950
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 agagacaggg tttctccatg ttggtcaggc tggctctcaa ctcccaacct 2050
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 ttactcctct ctctcccttg ttattcagtg tgaccaggat ggcggggagg 2250
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235
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 tgttccaaaa tggcatctta ctttatgga gtactctttg ctgttggcct 100
 ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
 ccgcctcttc ctccacaaag agcacccttg cctcacaggt gtattccctc 200
 aacaccgact ttgccttcgc cctataccgc aggtgtggtt tggagacccc 250
 gagtccagaa atcttcttct cccctgtgag tgtctcact tccctggcca 300
 tgccttcctt tggggccac tcagtcaaca agaccagat tctccagggc 350
 ctgggcttca acctcacaca cacaccagag tctgccatcc accagggtt 400
 ccagcacctg gttcactcac tgaactgttc cagcaaagac ctgaccttga 450
 agatgggaag tgcctcttc gtcaagaagg agctgcagct gcaggcaaat 500
 ttcttgggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550
 ttttccaac ccctccattg ccaggcgag gatcaacagc catgtgaaa 600
 agaagacca aggaaggtt gttagacataa tccaaggcct tgaccttctg 650
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 gccctttcac cttgaatata caagaaagaa cttccattc ctggtgggag 750
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 tttgggtgg atacagagct gaactgcttt gtgctgcaga tggattacaa 850
 gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900
 aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950
 ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
 ctctacaat ctggaacca tctctccgaa gatgggcac caaatgcct 1050
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 tgaggccaca gcagctacca ccaccaagtt catagtccga tcgaaggatg 1200
 gtccctctta cttcactgtc tcttcaata ggaccttct gatgatgatt 1250
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 tgcacaagaa ataacaacc acatccctct ttctgttctg aggtgtcatt 1400
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aatcaccaaa ccatcaacag ggaccccaagt cacaagcCaa caccattaa 1500
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 ggatgttgct gggttaccat atttcattc ctggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataacac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20					25					30
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35					40					45
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50					55					60
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65					70					75
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80					85					90
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95					100					105
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110					115					120
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125					130					135
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140					145					150
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155					160					165
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170					175					180
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185					190					195
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

	200		205		210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe		
	215	220	225		
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met		
	230	235	240		
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu	Asn		
	245	250	255		
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe		
	260	265	270		
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala		
	275	280	285		
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys		
	290	295	300		
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser		
	305	310	315		
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala		
	320	325	330		
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser		
	335	340	345		
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser		
	350	355	360		
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile		
	365	370	375		
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn		
	380	385	390		
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile		
	395	400	405		
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser			
	410	415			

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 238
 ctttgcgtgtt ggctctgtg ctcccaacca tgcaaggaca gggcag 47

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 239
 tgactcgggg tctccaaaac cagc 24

 <210> 240
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 240
 ggtataggcg gaaggcaaag tcgg 24

 <210> 241
 <211> 48
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

 <400> 241
 ggcaccttac ctttatggag tactctttgc tgttgccctc tgtgctcc 48

 <210> 242
 <211> 2436
 <212> DNA
 <213> Homo sapiens

 <400> 242
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 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
 aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga 350
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
 agtggggta gcacagccac catctcaggg tccagcgtga cctccaatgg 450
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 aatactatat tgctcattta gctaagaaat aaatacatct catctaacc 2250
 acacgacaaa gagaagctgt gcttgccccc ggtgggtat ctagtctga 2300
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

Thr Asn Ser Glu Ser Ser Thr Thr Val Ser Ser Gly Ala Ser Thr Ala	365	370	375
380	385	390	
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala			
395	400	405	
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala			
410	415	420	
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala			
425	430	435	
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val			
440	445	450	
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala			
455	460	465	
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala			
470	475	480	
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala			
485	490	495	
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile			
500	505	510	
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe			
515	520	525	
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn			
530	535	540	
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly			
545	550	555	
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro			
560	565	570	
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile			
575	580	585	
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro			
590	595		

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic sequence.

<400> 245
 gtcagagttg gtggctgtgc tagc 24

<210> 246
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 246
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 247
 gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50
 ttcccgacct tccagcaat atgcatcttg cagctctggt cggctcctgc 100
 tccctccttc tgctactggg ggcctgtct ggaaggcgcc ccagcgatga 150
 cccattgag aaggtcattg aagggatcaa ccgagggctg agcaatcgac 200
 agagagaggt gggcaaggcc ctggatggca tcaacatgg aatcacgcat 250
 gccgaaggg aagtggagaa ggttttcaac gaacttagca acatggggag 300
 ccacaccggc aaggagtgg acaaaggcgt ccaggggctc aaccacggca 350
 tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaa 400
 gaagcagaga agcttgcca tggggccaac aacgctgctg gacaggccgg 450
 gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtcaccagg 500
 ctgggaagga agcagagaaa cttgccaag gggtaacca tgctgctgac 550
 caggctggaag aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
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 acatcatgcc ctaaactggc atccggcctt gctggggagaa taatgtcgcc 850
 gttgtcaat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaat ccctgaaggg ggttgtagtg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat ctgtcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttccttct ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggtca ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252
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 tgacctgac tcactccagg tcggaggcg ggggccccg ggcgactcg 150
 ggggcggacc gcggggcgga gctgccgcc gtgagtccg ccgagccacc 200
 tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250
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 cctcgccac cgctgctgct gctcctgctg ctgctgctcc tgetgcagcc 350
 gccgcctccg acctgggcgc tcagccccg gatcagcctg cctctgggt 400
 ctgaagagcg gccattctc agattcgaag ctgaacacat ctccaactc 450
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 gcgccctca ccaggtcctg ggctcggacc caactcctgg acctttccag 3400
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 actctaaggg atatcaacac tgcccagcac aggggccctg aatttatgtg 3700
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 gctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80										85										90									
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr															
				95						100				105															
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys															
				110					115					120															
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile															
				125					130					135															
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly															
				140					145					150															
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn															
				155					160					165															
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp															
				170					175					180															
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala															
				185					190					195															
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe															
				200					205					210															
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro															
				215					220					225															
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe															
				230					235					240															
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly															
				245					250					255															
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu															
				260					265					270															
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile															
				275					280					285															
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp															
				290					295					300															
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp															
				305					310					315															
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro															
				320					325					330															
Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr															
				335					340					345															
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val															
				350					355					360															
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys															
				365					370					375															

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His Pro
380	385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala Arg
395	400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln Leu	Pro Asp Arg Val Leu
410	415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg Ser
425	430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val Ala
440	445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu Phe
455	460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val Gly
470	475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser Gly
485	490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu Leu
500	505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala Asn
515	520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg Asp
530	535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser Leu
545	550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile Glu
560	565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val Ser
575	580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val Gln
590	595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu Ser
605	610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val Asn
620	625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu Leu
635	640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu Glu
650	655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val Val

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro	
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys	
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val	
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe	
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln	
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val Leu	
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr	
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro	
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile	
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg	
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp	Ser Val Val	
830	835	

<210> 254

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 254

agcccggtgca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 255
 tgaagccagg gcagcgtcct ctgg 24

<210> 256
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 256
 gtacaggctg cagttggc 18

<210> 257
 <211> 41
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

<400> 257
 agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 258
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<210> 259
 <211> 4563
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> unknown base

<400> 259
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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				20					25					30
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Ala	Ser	Pro	
				35					40					45
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
				50					55					60
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
				65					70					75
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
				80					85					90
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
				95					100					105
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
				110					115					120
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
				125					130					135
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
				140					145					150
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
				155					160					165
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
				170					175					180
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
				185					190					195
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
				200					205					210
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
				215					220					225
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
				230					235					240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val
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Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser
260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys
275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala
290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu
305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg
320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser
335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro
350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu
365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly
380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu
395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala
410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly
425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp
440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val
455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile
470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys
485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser
500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu
515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile Asn	Ile Leu Ile Pro Leu

530										535										540									
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				545										550															
Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu															
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Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu															
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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln															
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Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys															
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Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg															
				635										640															
Ala	Asn	Thr	Val	Leu	Gly	Gln	Gln	Ile	Tyr	Phe	Pro	Ile	Ile	Phe															
				650										655															
Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser															
				665										670															
Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn															
				680										685															
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg															
				695										700															
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp															
				710										715															
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe															
				725										730															
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe															
				740										745															
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly															
				755										760															
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met															
				770										775															
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn															
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Asn	Gly	Ser	Val	Arg	Thr	Ala																							
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<210> 261

<211> 24

<212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 261
 gtgccactac ggggtgtgga cgac 24

<210> 262
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 262
 tcccatttct tccgtggtgc ccag 24

<210> 263
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

<400> 263
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<210> 264
 <211> 1419
 <212> DNA
 <213> Homo sapiens

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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25				30	

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35				40					45	

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	65		70		75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80		85		90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95		100		105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110		115		120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125		130		135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140		145		150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155		160		165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170		175		180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185		190		195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200		205		210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215		220		225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230		235		240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245		250		255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260		265		270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275		280		285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290		295		300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305		310		315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320		325		330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335		340		345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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 caaattaaac taaacaatat atttaaagat gatataaac tactcagtg 2300
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<210> 267
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 267
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Leu Val Gly Glu	Asp Ala Val Phe Ser Cys	Ser Leu Phe Pro	Glu Glu
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Thr Ser Ala Glu	Ala Met Glu Val Arg Phe	Phe Arg Asn Gln Phe	
	50	55	60
His Ala Val Val	His Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser	
	65	70	75
Lys Gln Met Pro	Gln Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp	
	80	85	90
Ser Ile Ala Gly	Gly Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr	
	95	100	105
Pro Ser Asp Ile	Gly Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile	
	110	115	120
Tyr Asp Glu Glu	Ala Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly	
	125	130	135
Ser Leu Pro Leu	Ile Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile	
	140	145	150
Gln Leu Leu Cys	Leu Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala	
	155	160	165
Lys Trp Lys Gly	Pro Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg	
	170	175	180
Ala Asn Ala Asp	Gly Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile	
	185	190	195
Ile Val Gln Glu	Asn Ala Gly Ser Ile Leu	Cys Ser Ile His Leu	
	200	205	210
Ala Glu Gln Ser	His Glu Val Glu Ser Lys	Val Leu Ile Gly Glu	
	215	220	225
Thr Phe Phe Gln	Pro Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu	
	230	235	240
Gly Leu Leu Cys	Gly Ala Leu Cys Gly Val	Val Met Gly Met Ile	
	245	250	255
Ile Val Phe Phe	Lys Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp	
	260	265	270
Trp Arg Arg Lys	His Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys	
	275	280	285
His Ala Val Glu	Val Thr Leu Asp Pro Glu	Thr Ala His Pro Lys	
	290	295	300
Leu Cys Val Ser	Asp Leu Lys Thr Val Thr	His Arg Lys Ala Pro	
	305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
				395					400					405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
				410					415					420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
				425					430					435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
				440					445					450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
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<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

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 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggctctt 250
 aacaatttta cagaaatgag ccagagactt gaatcaatg tgaaaaatgc 300
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 agttcagtca acagaagcat ggagtggttg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggacccctc aaagtagatc 500

ctactcagct taaaattaaa aaaatcaaca agacagaaac agacagctat 550
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
 caggatcgtt ggtgggacag aagtagaaga gggatgaatgg cctgggcagg 650
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 aataccaatc acttcatcat ttaggaagta tgggaactaa gtttaaggaag 1900
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 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

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				20					25					30
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr
				35					40					45
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr
				50					55					60
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn
				65					70					75
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala
				80					85					90
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val
				95					100					105
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu
				110					115					120
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp
				125					130					135
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val
				140					145					150
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile
				155					160					165
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr
				170					175					180
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly
				185					190					195
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln
				200					205					210
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr
				215					220					225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
 395 400 405
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
 410 415 420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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 ttccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

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<210> 271
 <211> 238
 <212> PRT
 <213> Homo sapiens

<400> 271
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 20 25 30
 Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
 35 40 45
 Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
 50 55 60
 Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
 65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
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<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

	170		175		180
Cys Cys Val Arg	Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln				
	185		190		195
Glu Asp Leu Ser	Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met				
	200		205		210
Tyr Ser Phe Leu	Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe				
	215		220		225
Leu Gly Ile Ser	Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu				
	230		235		240
Thr Ile Thr Leu	Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Phe				
	245		250		255
Gly Thr Asp Gln	Met Met Ser Leu Lys Asn Asp Asn Ser Gln His				
	260		265		270
Leu Ser Cys Pro	Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg				
	275		280		285
Ile Phe Glu His	Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe				
	290		295		300
Glu Met Glu Glu	Leu				
	305				

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 ttctgacctg ctggccagcc aggcctgtg tggggaggcc ctctgctgc 150
 cttgggtga caatctcagc tccaggctac agggagatcg ggaggatcac 200
 agagccagca tggtacagga tctgcacagt gatcaactc tgaacagcct 250
 cgatgtcaaa cccctgcga aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcac atagcactac tgagcctggc gactatcac 350
 attgtggtg tctcatcaa ggtgattctg gataatact acttccctg 400
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
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Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
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Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
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Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
			80						85					90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
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Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
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Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
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Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
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Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
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Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
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Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
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Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
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Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
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Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
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Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
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Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
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 275 280 285
 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
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 Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305 310 315
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
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 Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
 335 340 345
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 350 355 360
 Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
 365 370 375
 Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 380 385 390
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
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 Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
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 425 430

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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 Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45
 Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60
 Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75
 Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90
 Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105
 Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120
 Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135
 Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150
 Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165
 Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180
 Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195
 Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210
 Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225
 Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255
 Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270
 Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285
 Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

	290		295		300
Phe Asn Val Ile	Arg His Ala Val	Leu Leu Pro Ala Asp Ser	Pro		
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Thr Ala Pro His	Ile Tyr Ala Val	Phe Thr Ser Gln Trp Gln	Val		
	320		325		330
Gly Gly Thr Arg	Ser Ser Ala Val	Cys Ala Phe Ser Leu Leu	Asp		
	335		340		345
Ile Glu Arg Val	Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys	Glu		
	350		355		360
Thr Ser Arg Trp	Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro	Arg		
	365		370		375
Pro Gly Ser Cys	Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu	Thr		
	380		385		390
Phe Met Lys Asp	His Phe Leu Met Asp	Glu Gln Val Val Gly	Thr		
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Pro Leu Leu Val	Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala	Val		
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Glu Thr Ala Gln	Gly Leu Asp Gly His	Ser His Leu Val Met	Tyr		
	425		430		435
Leu Gly Thr Thr	Thr Gly Ser Leu His	Lys Ala Val Val Ser	Gly		
	440		445		450
Asp Ser Ser Ala	His Leu Val Glu Glu	Ile Gln Leu Phe Pro	Asp		
	455		460		465
Pro Glu Pro Val	Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly	Ala		
	470		475		480
Val Phe Val Gly	Phe Ser Gly Gly Val	Trp Arg Val Pro Arg	Ala		
	485		490		495
Asn Cys Ser Val	Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala	Arg		
	500		505		510
Asp Pro His Cys	Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys	Leu		
	515		520		525
Leu Ser Ala Pro	Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu	Arg		
	530		535		540
Gly Asn Pro Glu	Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg	Ser		
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Leu Arg Pro Gln	Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu	Ala		
	560		565		570
Val Pro Asn Ser	Ile Leu Glu Leu Pro	Cys Pro His Leu Ser	Ala		
	575		580		585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
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Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
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Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
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Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
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Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
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<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

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<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279
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<210> 280
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 280
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<210> 281
 <211> 2320
 <212> DNA
 <213> Homo sapiens

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 ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300
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 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

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Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
			35						40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
			50						55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
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Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
			80						85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
			95						100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
			110						115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
			125						130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
			140						145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
			155						160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
			170						175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
			185						190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
			200						205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
			215						220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
			230						235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
			245						250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys	Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn
275	280	285
Phe Ile Ala Lys	Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu
290	295	300
Gly Ser Met Val	Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu
305	310	315
Met Asn Asn Ala	Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys
320	325	330
Cys Gln Cys Ser	His Trp Pro Lys Asp	Val His Leu Ala Ala Asn
335	340	345
Val Lys Ile Val	Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His
350	355	360
Pro Ser Ile Arg	Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile
365	370	375
Met Glu Ala Ile	Gln His Gly Val Pro	Met Val Gly Ile Pro Leu
380	385	390
Phe Gly Asp Gln	Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys
395	400	405
Phe Gly Val Ser	Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu
410	415	420
Ala Leu Lys Met	Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser
425	430	435
Ala Ala Val Ala	Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser
440	445	450
Pro Thr Gln Arg	Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr
455	460	465
Gly Gly Ala Thr	His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp
470	475	480
His Glu Gln Tyr	Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu
485	490	495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala
500	505	510
Val Trp Trp Leu	Arg Gly Ala Arg Lys	Val Lys Glu Thr
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 283
 tgcctttgct cacctacccc aagg 24

 <210> 284
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 284
 tcaggctggt ctccaaagag aggg 24

 <210> 285
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 285
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

 <210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

 <400> 286
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
 ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
 cccgtcacac acacatacca tggtctccat cccccagggt ccagccctca 150
 gtgctgtccc atccagcagg gctaccctga agctctgggt gcagccctcc 200
 cgtccagtgg gcaggcgggt tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcatgctctg ccaaggagga ggaactgca gtgacagcag 300
 gagtaagagt gggaggcagg acagagctgg gacacaggtg tggagagggg 350
 gttcagcgag cctagagagg gcagactatc aggggtgccg cggtgagaat 400
 ccagggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgacaga gccctcagc catgttggga gccaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550
 tgggggcgag gtgggccag gaggggtcag agcccgtcct gctggagggg 600
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 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctgggtg aacgaggggc gtggctttga 800
 cggggcctct ggctccttcg tagccctgtg ccgggggtgc tacagcttcc 850
 ggttccatgt ggtgaagtg tacaaccgcc aaactgtcca ggtgagcctg 900
 atgtctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950
 gaccgggag gcagccacca gctctgtgct actgcccttg gacctgggg 1000
 accgagtgtc tctgcgctg cgctggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttcttctg cctctcttg 1150
 cccagaaac agcagaggca ggagagagac tccctctggc tccatccca 1200
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250
 gagctgtggc atctccagac caggccttcc caccaccca ccccgagta 1300
 cctcccgag cactgtctgc atctgttccg gctgcagcc ctaggatcag 1350
 ggcaaggttt ggcaagaag aagatctgca ctactttgcg gcctctgtct 1400
 ctccggttcc cccacccag ctctctgtct aatgctgac agggacaggt 1450
 ggcgaggtg agcctgacag gcccccacag gagccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttctctgtgag gaaagccagc atcacggatc 1550
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 aggctcagcc acaggcagaa ggggtgggaag ggcttgaggt ctgtggctgg 1650
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 gctggtatcc agatggactc tggcccttac ctccccacct gagattaggg 1800
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag ttgaaacttt agtccctcca 1950
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 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
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 cattctctta gacctctccc tgccagtatg ctaaacccctc cctctctctt 2150
 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atgggtggta gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgtaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser	1	5	10	15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly	20	25	30	
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys	35	40	45	
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Gly	Gly	Pro	Gly		50	55	60	
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala	65	70	75	
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	80	85	90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	95	100	105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	110	115	120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	125	130	135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	140	145	150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	155	160	165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser				

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggcgccc ggccgcagct ccaggtgtcc 50
 tagccgccca gctcgaagc cgtcccggga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggtcctg cgcggcgagc gtcaggccga ggtctgaccg 250
 agccagcgct ctacggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tctctccgc cctccaggac ctcttctctg 350
 tcacctggct caataggtcc aagtggaag agcagctaca ggtcatctca 400
 gtgtccagt gggctctgtc ctctcttcta ctgggagtg cctgcagtgc 450
 catcctcatg tacatattct gcactgattg ctggctcacc gctgtgctct 500
 acttcacttg gctgtgttt gactggaaca caccaagaa aggtggcagg 550
 aggtcacagt gggtcgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctggtga agacacacaa cctgctgacc accaggaaat 650
 atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700
 aacttcagca cagagggcac agaagtgagc aagaagtcc caggcatacg 750
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
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 ctggttccca tctactcctt tggagagaat gaagtgtaca agcagggtgat 1050
 cttcgaggag ggctcctggg gccgatgggt ccagaagaag ttccagaaat 1100
 acattgtgtt cgcctcatgc atcttccatg gtcgaggcct cttctcctcc 1150
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 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
 acctgtacca caccatgtac atggaggccc tgggtgaagct ctcgacaaag 1300
 cacaagacca agttcgccct cccggagact gaggtccttg aggtgaactg 1350
 agccagcctt cggggccaat tcctggagg aaccagctgc aaatcatctt 1400
 ttgtctctgt aaatttgtaa gtgtcatggg tgtctgtggg ttatttataa 1450
 gaaattataa caattttgct aaacaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

	260		265		270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr				
	275		280		285
Lys Gln Val Ile	Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln				
	290		295		300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His				
	305		310		315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr				
	320		325		330
Ser Lys Pro Ile	Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro				
	335		340		345
Lys Leu Glu His	Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr				
	350		355		360
Met Tyr Met Glu	Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr				
	365		370		375
Lys Phe Gly Leu	Pro Glu Thr Glu Val Leu Glu Val Asn				
	380		385		

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tctctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50
ccgacgcagc gccggggccg gccaggggcc gaggagcgcg gcgccagag 100
cggggccgcg gaggcgacgc cggggagcgc cgcgcgacga gcagggtggc 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttccact 200
ggctctgctg accttgtgcc ttgacggct gtctcagcg aggggcccgtg 250
caccgcctcc tgagcagcgc catgggctg ctggccttcc tgaagaccac 300
gttcgtgctg cacctgctgg tcgctttgt cttcgtggtg agtggctcgtg 350
tcatcaactt cgtccagctg tgacgcctg cgtctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgcgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtcctg caggagtggt acactgttca 500
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ttccaggagg agcagtttaa gcttgcggg aggcgtgga cctcctgaa 1200
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 tttgtgggag cagcttcctt tggagttcgc agactgatg gagaatcgt 1350
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 ccagcctagg caacagagca agactcagtc tcaaaaaaa aaaaaacaa 1450
 aaaaaccca gaaattcttg agttgaactg tgtagttact gacatgaaa 1500
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550
 agcttgaga tggtacctg agatttttca ggctaataa aaaagaatga 1600
 aggaaaatta acagcctcag agaccatgg tgcaccgtca cacaataca 1650
 catatgcatg atgagagtc cagaaggaga ggagagaaa ggtcagaaa 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
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 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
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 aagcttctct gacctgtagg aaggcctgtc tttaggccg gcacagtggc 2100
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 ggggtcaggc tgatctcaa ctccagagtt cagggtatct gccgcctca 2200
 gcctccaaa gtgttgatg tgcaggcgtg agccactgag cctggccgga 2250
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 gtgatccaa gtagcttggg ttgtaaacat gcaccacat gctggctaa 2350
 tttttgtatt tttagtagag acgtgttagc caggctggtc tcatctct 2400
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 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500
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ttgttcgtt gccagggctg gactacagtg gcacagcttt ggctcactgc 2650
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 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaat gggcagaggg gccgggtgtg gccccaacta 2950
 ccaggagac tgaagtggga ggcacgcttg ggcagagaa gtcgaggctg 3000
 cagtgaagtc aggttgtgcg actgcattcc agcctggaca acagagttag 3050
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
 170 175 180
 Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
 185 190 195
 Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
 200 205 210
 Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
 215 220 225
 Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 230 235 240
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
 245 250 255
 Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
 260 265 270
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
 275 280 285
 Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
 290 295 300
 Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
 305 310 315
 Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
 320 325 330
 Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
 335 340 345
 Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
 350 355 360
 Glu Pro Gly Arg Trp Arg Leu Gln
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<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

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<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

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<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tcagttgtc ttgtggggtt ggtggcaggc aggccgctt acgcctgata 200
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gttgtatggg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750

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 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
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 acagagtggag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130					135

Cys Gly Val Leu Leu Ser Phe Leu

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
				20					25				30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40				45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55				60	

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
 65 70 75
 Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
 80 85 90
 Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
 95 100 105
 Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
 110 115 120
 Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
 125 130 135
 Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
 140 145 150
 Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
 155 160 165
 Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
 170 175 180
 Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
 185 190 195
 Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
 200 205 210
 Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
 215 220 225
 Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
 230 235 240
 Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
 245 250 255
 Leu Thr Leu Ala Phe Lys Ile
 260

<210> 307
 <211> 2272
 <212> DNA
 <213> Homo sapiens

<400> 307
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 ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe		
			35					40						45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
			50					55						60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
			65					70						75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
			80					85						90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
			95					100						105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
			110					115						120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
			125					130						135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Ser	Asp	Ser	Lys	Ser	Ser

140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met Ser	
155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln Ala	
170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser	Glu Ser Ser Ser Glu	
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr	Pro Glu Lys Lys Ala	
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu	Gly Gly Arg Lys Lys	
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp	Ser Lys Ala Asp Ser	
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met	Ala Arg Ser Ala Ser	
245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp	Ser Asp Val Ser Val	
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala	Glu Lys Pro Leu Pro	
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu	Arg Pro Pro Ser Ser	
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val	Asp Arg Ile Ser Glu	
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg	Glu Leu Glu Ala Arg	
320	325	330
Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg	Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu	Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser	Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg Gly	Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu	Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys	Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys	Glu Lys Arg Val Arg	
425	430	435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
 440 445 450
 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
 455 460 465
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
 470 475 480
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
 485 490 495
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
 500 505 510
 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
 515 520 525
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
 530 535 540
 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
 545 550 555
 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
 560 565 570
 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
 575 580 585
 Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
 590 595 600
 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
 605 610 615
 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
 620 625 630
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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 Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
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 665 670

<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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				20					25					30
Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35					40					45
Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro
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Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65					70					75
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile

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Tyr Trp Pro Ala	Ala Lys Glu Arg Val Glu Leu Cys Lys Leu Ala		
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Gly Lys Asp Ala	Asn Thr Glu Cys Ala Asn Phe Ile Arg Val Leu		
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Gln Pro Tyr Asn	Lys Thr His Ile Tyr Val Cys Gly Thr Gly Ala		
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Phe His Pro Ile	Cys Gly Tyr Ile Asp Leu Gly Val Tyr Lys Glu		
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Asp Ile Ile Phe	Lys Leu Asp Thr His Asn Leu Glu Ser Gly Arg		
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Leu Lys Cys Pro	Phé Asp Pro Gln Gln Pro Phe Ala Ser Val Met		
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Thr Asp Glu Tyr	Leu Tyr Ser Gly Thr Ala Ser Asp Phe Leu Gly		
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Lys Asp Thr Ala	Phe Thr Arg Ser Leu Gly Pro Thr His Asp His		
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His Tyr Ile Arg	Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly		
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Ala Lys Phe Ile	Gly Thr Phe Phe Ile Pro Asp Thr Tyr Asn Pro		
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Asp Asp Asp Lys	Ile Tyr Phe Phe Phe Arg Glu Ser Ser Gln Glu		
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Gly Ser Thr Ser	Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val		
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Cys Lys Asn Asp	Val Gly Gly Gln Arg Ser Leu Ile Asn Lys Trp		
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Asp Gly Ala Asp	Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu		
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Leu Pro Thr Arg	Asp Glu Arg Asn Pro Val Val Tyr Gly Val Phe		
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Ser Met Ala Asp	Ile Arg Ala Val Phe Asn Gly Pro Tyr Ala His		
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 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

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Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu					
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 <213> Artificial

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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

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<212> PRT
<213> Homo sapiens

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Pro Ser Ile Glu Gln	Arg Leu Gln Glu Val	Arg Glu Ser Ile Arg	50	55	60
Arg Ala Gln Val Ser	Gln Val Lys Gly Ala	Ala Arg Leu Ala Leu	65	70	75
Leu Gln Gly Ala Gly	Leu Asp Val Glu Arg	Trp Leu Lys Pro Ala	80	85	90
Met Thr Gln Ala Gln	Asp Glu Val Glu Gln	Glu Arg Arg Leu Ser	95	100	105
Glu Ala Arg Leu Ser	Gln Arg Asp Leu Ser	Pro Thr Ala Glu Asp	110	115	120
Ala Glu Leu Ser Asp	Phe Glu Glu Cys Glu	Glu Thr Gly Glu Leu	125	130	135
Phe Glu Glu Pro Ala	Pro Gln Ala Leu Ala	Thr Arg Ala Leu Pro	140	145	150
Cys Pro Ala His Val	Val Phe Arg Tyr Gln	Ala Gly Arg Glu Asp	155	160	165
Glu Leu Thr Ile Thr	Glu Gly Glu Trp Leu	Glu Val Ile Glu Glu	170	175	180
Gly Asp Ala Asp Glu	Trp Val Lys Ala Arg	Asn Gln His Gly Glu	185	190	195
Val Gly Phe Val Pro	Glu Arg Tyr Leu Asn	Phe Pro Asp Leu Ser	200	205	210
Leu Pro Glu Ser Ser	Gln Asp Ser Asp Asn	Pro Cys Gly Ala Glu	215	220	225
Pro Thr Ala Phe Leu	Ala Gln Ala Leu Tyr	Ser Tyr Thr Gly Gln	230	235	240
Ser Ala Glu Glu Leu	Ser Phe Pro Glu Gly	Ala Leu Ile Arg Leu	245	250	255
Leu Pro Arg Ala Gln	Asp Gly Val Asp Asp	Gly Phe Trp Arg Gly	260	265	270
Glu Phe Gly Gly Arg	Val Gly Val Phe Pro	Ser Leu Leu Val Glu	275	280	285
Glu Leu Leu Gly Pro	Pro Gly Pro Pro Glu	Leu Ser Asp Pro Glu	290	295	300
Gln Met Leu Pro Ser	Pro Ser Pro Ser Phe	Ser Pro Pro Ala			

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Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met	Ala Pro		
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 cttcatctcc caaagtgtg ggattacagg cgtgagccac cgtgcctggc 4000
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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg
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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
			20						25					30
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
			35						40					45
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu

	140		145		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	155	Leu His Leu Gln Pro Leu	165		
Glu Gly Gly Thr Pro Asn Ser Ala Gly	170	Gly Pro Gly Ala His Ile	180		
Leu Arg Arg Lys Ser Pro Ala Ser Gly	185	Gln Gly Pro Met Cys Asn	195		
Val Lys Ala Pro Leu Gly Ser Pro Ser	200	Pro Arg Pro Arg Arg Ala	210		
Lys Arg Phe Ala Ser Leu Ser Arg Phe	215	Val Glu Thr Leu Val Val	225		
Ala Asp Asp Lys Met Ala Ala Phe His	230	Gly Ala Gly Leu Lys Arg	240		
Tyr Leu Leu Thr Val Met Ala Ala Ala	245	Ala Lys Ala Phe Lys His	255		
Pro Ser Ile Arg Asn Pro Val Ser Leu	260	Val Val Thr Arg Leu Val	270		
Ile Leu Gly Ser Gly Glu Glu Gly Pro	275	Gln Val Gly Pro Ser Ala	285		
Ala Gln Thr Leu Arg Ser Phe Cys Ala	290	Trp Gln Arg Gly Leu Asn	300		
Thr Pro Glu Asp Ser Gly Pro Asp His	305	Phe Asp Thr Ala Ile Leu	315		
Phe Thr Arg Gln Asp Leu Cys Gly Val	320	Ser Thr Cys Asp Thr Leu	330		
Gly Met Ala Asp Val Gly Thr Val Cys	335	Asp Pro Ala Arg Ser Cys	345		
Ala Ile Val Glu Asp Asp Gly Leu Gln	350	Ser Ala Phe Thr Ala Ala	360		
His Glu Leu Gly His Val Phe Asn Met	365	Leu His Asp Asn Ser Lys	375		
Pro Cys Ile Ser Leu Asn Gly Pro Leu	380	Ser Thr Ser Arg His Val	390		
Met Ala Pro Val Met Ala His Val Asp	395	Pro Glu Glu Pro Trp Ser	405		
Pro Cys Ser Ala Arg Phe Ile Thr Asp	410	Phe Leu Asp Asn Gly Tyr	420		
Gly His Cys Leu Leu Asp Lys Pro Glu	425	Ala Pro Leu His Leu Pro	435		

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
 440 445
 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
 500 505 510
 Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
 515 520 525
 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
 530 535 540
 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
 605 610 615
 Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
 695 700 705
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

	725		730		735
Tyr Ala Leu Asn	Gly Glu Tyr Thr Leu	Met Pro Ser Pro Thr Asp			
	740	745		750	
Val Val Leu Pro	Gly Ala Val Ser Leu	Arg Tyr Ser Gly Ala Thr			
	755	760		765	
Ala Ala Ser Glu	Thr Leu Ser Gly His	Gly Pro Leu Ala Gln Pro			
	770	775		780	
Leu Thr Leu Gln	Val Leu Val Ala Gly	Asn Pro Gln Asp Thr Arg			
	785	790		795	
Leu Arg Tyr Ser	Phe Phe Val Pro Arg	Pro Thr Pro Ser Thr Pro			
	800	805		810	
Arg Pro Thr Pro	Gln Asp Trp Leu His	Arg Arg Ala Gln Ile Leu			
	815	820		825	
Glu Ile Leu Arg	Arg Arg Pro Trp Ala	Gly Arg Lys			
	830	835			

<210> 318

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 319

ctgtgctctt cggcgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttgta tcttggcctt aactctaatt gtcctgtttt 200
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaat ggcatgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcatg atttgggtcc cagcagaaaa gcctattgaa 550
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tgttctaata aacttctaca ttatcaccaa aaaaaaaaa aaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285
 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300
 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315
 Arg Val

<210> 323
 <211> 1174
 <212> DNA
 <213> Homo sapiens

<400> 323
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ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
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 gtttggtcag tgggggttgg ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324
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 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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 gcatcgcggc caccgggatg gacatgtgga gcaccaggga cctgtacgac 200
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 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tggtcgagac tgttcagacc aggtacacat 600
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 aggttaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

	80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg			
	95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr			
	110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly			
	125	130	135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser			
	140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val			
	155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val			
	170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala			
	185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser			
	200	205	210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe			
	215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile			
	230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro			
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Ser Lys His Asp Tyr Val			
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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 taagggtggt caagcatcta ctctttttat catttaacttc aaaatgacat 1050
 tgctaagac tgcattatit tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctccacataga gacatgctta 1150
 tatggtttta ttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
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 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagtgtg 1750
 cctttgagaa ctccacctgc tctatgtgg gtacctgagt caaaattgtc 1800

attttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgtttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtgcacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc ttatataatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
 215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacaactg 50
 ctgggctggg tgaatggcct ggtctctctgt gccctgccca tgtggaaggt 100
 gaccgctttc atcggaaca gcatcgtggt gggccagggt gtgtgggagg 150
 gcctgtggat gtctgcgtg gtgcagagca cggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gtctggcttg ctggtctacc 300
 ttgtctgggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgctgggtgc tcacctctgg gattgtcttt gtcattctcag gggctctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggt ggtgagggc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgcgtg 550
 ctgcacttgc cctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtacctc 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
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 ttttgtttct gccctctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaat actgagccaa ggtgttgact cagactctca cttaggctct 850
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 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
 tgcggaggct gcttgcgtg ctggccttgc aacaagacag actgtcccca 1000
 agagtctctg ctgctgctgg gggctgggct tcctagatg tcaactggaca 1050
 gctgcccccc atctactca ggtctctgga gctctctctc tcacctggt 1100
 aaaaacaaat catctgttaa caaaggactg cccacctcag gaacttctga 1150
 cctctgtttc ctccgtctg ataagacgtc cccccccag ggccaggctc 1200
 cagctatgta gacccccgcc ccacctcca acactgcacc cttctgccct 1250

gcccccctcg tctcaccccc tttaactca catttttatc aaataaagca 1360

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
			35						40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
			50						55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
			65						70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
			80						85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
			95						100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
			110						115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
			125						130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
			140						145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Trp
			155						160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Gly	Gly	Gly	Leu	
			170						175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
			185						190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
			200						205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val					
			215						220					

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agactttctt agactcaaaa ggcttccacg 50
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatctta tcccttgcaa attgctgggc tggttcttgg 150
gttctctggc atgggtggga ctcttgccac aacccttctg cctcagtggt 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggtc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgctgcctt ggaacagcc 350
cgggccctca tgtgtgtggc tgttgcctc tccttgatcg cctgtcttat 400
tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcacagaga 550
ttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
cacttttctt tggctgggca agcgtgctgt tcctcttcat tggagggggg 650
ctgctttgtg gattttgtg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaagcct ccttttggct 800
ccaagtatgg actatgggtc atgtttttta taaagtcctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtctt aatttgttac tgggtgtagg aatgaaaaatg acttacttgg 950
acattctgac ttcagggtga ttaaatgcat tgactat'tgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaagttg aaattgatat tctatacaaa taaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu	Leu Ala Leu Pro Pro Ala	Leu Glu Thr Ala Arg	
	20	25	30
Ala Leu Met Cys Val	Ala Val Ala Leu Ser Leu Ile Ala Leu Leu		
	35	40	45
Ile Gly Ile Cys Gly	Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
	50	55	60
Glu Arg Ala Lys Ala	Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
	65	70	75
Ile Leu Thr Gly Ile	Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
	80	85	90
Asn Ile Ile Ile Arg	Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
	95	100	105
Gln Lys Arg Glu Leu	Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
	110	115	120
Ala Ala Val Leu Phe	Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
	125	130	135
Cys Cys Asn Arg Lys	Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
	140	145	150
Tyr Arg Val Pro His	Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
	155	160	165
Ser Lys Thr Ser Thr	Ser Tyr Val		
	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtggtagcc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcaact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggcctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgccg gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgccg cccgcgcgca tggctgcctc cccgcgcg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tctgtgtctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaa gagaaagacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttgccag cctgaagcgc cagaagcggc agctgtggga ccgactcgg 300

cccgaggctg agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccgagagccc ctacggcttt aggcgatggag ccagcgtcaa 500

ctacgatgac tactaacat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tccaatgcc ttacactact tggtttctga 600

tttgccttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct ttgatattt catgggaatg 700
cctctcattt aaaaatagaa ataaagcatt tigttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
1				5					10					15
Leu	Ala	Leu	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser
				20					25					30
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
				35					40					45
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
				50					55					60
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65					70					75
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80					85					90
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95					100					105
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110					115					120
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125					130					135
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr		
				140					145					

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

cggtctgagc ccgcccgaa gtgcccgagg gcccgcatg gagctggggg 50
agccgggagc tcggtagcgc gccgggcaag gcaggcgcca tgacctgat 100
tgaaggggtg ggtgatgagg tgaccgtcct tttctcgtg cttgcctgcc 150
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgaggcgagg 200
gacctactgc cccagccgtc agggacccca acgccatccc agcccgagc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcagc 350
 ggggttcacag caacaccgcc agccccggac tccccgcagg agccccctgt 400
 gctacggctg aaattctctc atgattcaga gcaggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtgtcc cggccgggaa 500
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcggtccc ccaaatcccc cctgcccgcc ggggtccgag 650
 ccggccctc cggggtgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttccctgac cgccactctg ggccctggcc gcttcacct gctcctcagt 800
 ctctggcct ttgccatgta ccgccgtag tgctcccgcg ggcgcttgcc 850
 agcgtcccg gccctccgg accttgctcc ccgcgcccg gcgggagctg 900
 ctgctgccc aggcccgct ctccggcctg cctcttccc ctgccctgga 950
 gccaccctc gcgccgaga ggaactcccg gactggcgga ggccccgcc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgcactggga gtgggtcct cggggtcggg catctgctgt cgctgctcgt 1100
 gccccgggca gagccgggcc gccccggggg ccgctcttag tgttctgcg 1150
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 acgccaggtc ggtgggaggc tgggtgaagg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaa 1300
 aaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 5 10 15
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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 tgcctctctc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacctca agaaccatca gccctcagct gcacctctc cctcccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagcttctc ttgccctaaa 200
 tcaggccagc ctcacagtc gctgtgactt ggcccagtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgacctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgctgaate ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gtccggagca cgggggatga acaactgggt agaattggagg ttgactgtgt 550
 caggccggcc actctcctac tggctgacag gatgcgcct gagatgaaac 600
 aggggtcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
 ggattcttca tttcttcttc ctactgcctc cacttcattgt tattttcttc 700
 ccttccatt tacaactaaa actgaccaga gcccaggaa taaatggttt 750
 tcttgcttc ctcttactc ccatctggac ccagtcacct ggttcctgtc 800
 tgtattttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 345
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<210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

<400> 346
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 aaggagaaaa ccggggtaaa gggagggaag caattcaatt tgaagtcct 200
 gtgaatgggc ttgcagaagg caattaaaga aatccactca gagaggactt 250
 ggggtgaaac ttgggtcctg tggttttctg attgtaagt gaagcaggtc 300
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 gcctggagcg ggagaaagct aactgaaca tgacctgttg catttggcaa 450
 gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly
260	265	270
Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His		
275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile		
290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile		
305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg		
320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro		
335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg		
350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr		
365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly		
380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly		
395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln		
410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg		
425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu		
440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala		
455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu		
470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu		
485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His		
500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp		
515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg		
530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe		

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala Val Arg Gln Glu Gln Val				
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln				
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met Ile Val His Ile Leu Ser				
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu				
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe				
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
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 ctacagacatg gagtcaggga tgtggcctgc gctgctgctg tcccacctcc 100
 tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgcctcagggc 150
 tcttcacct cccctcgaac cccaccagcc ccagcccgcc ccccggtgctc 200
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 cctggcactg cccccccagc ccccccatca ggctttgagg agggggccgc 350
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 aggatggagg ggacccaac tctgccaatc ccgatttctt ggactatggt 450
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 tcaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

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1

5

10

15

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 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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 tcgccgcct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccgcc 450
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<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Val	Ser
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Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln
				20					25				30
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser
				35					40				45
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val
				50					55				60
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp
				65					70				75
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly
				80					85				90
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr
				95					100				Cys
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser
				110					115				120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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gtgctgacg gcggcgctgg cccacggctg tctgactgc cacagcaact 150
 tctccaagaa gttctcttc taccgccacc atgtgaactt caagtctctg 200
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
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 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1				5					10					15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
				20					25					30
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
				35					40					45
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
				50					55					60
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
				65					70					75
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
				80					85					90
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
				95					100					105
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
				110					115					120
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln
				125					130					135
Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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 cagaagttaa aggctgtctc caagtcctcg aactcagcag aaatagacca 1450
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<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
			200						205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
			215						220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
			230						235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
			245						250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
			260						265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgcc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-20
 <223> Synthetic construct.

<400> 360
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<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
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<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggtacagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
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agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcgccg gcgcttgggg 250
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ttcgtggcaa atggtacaca agggaaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagcttc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
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 attagcaag gataaatgcc gaaggctcact tcattctgga cacagttgga 1700
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 cgtggagagt aaaaagtatc gggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1				5			10					15
Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Leu	Gly
				20					25			30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Thr	Pro	Lys
				35					40			45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys
				50					55			60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser
				65					70			75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe
				80					85			90
Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe
				95					100			105

Arg Ile Ser Trp Ala Gly Asp Leu Asp	Lys Lys Asp Ala Ser Ile
110	115 120
Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys	
125	130 135
Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile	
140	145 150
Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val	
155	160 165
Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr	
170	175 180
Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn	
185	190 195
Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser	
200	205 210
Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly	
215	220 225
Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile	
230	235 240
Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile	
245	250 255
Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn	
260	265

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
aggggcgcgg ccccggcgca gtccccgcg gcccccgacc ctgaggcgctc 250
gcctctggcc gagccgccac aggagcagtc cctcgccccc tggctctccg 300
agaccccgcc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agcccgacc tgctgcacag gatcaaggat gaggtgggag caccgggcat 400
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gttatgtga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

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cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
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 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
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<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val	350	355	360
Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg	365	370	

<210> 367

<211> 30
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-30
 <223> Synthetic construct.

 <400> 367
 tggaaaagaa gtctgtgcag aaggtttagg 30

 <210> 368
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 368
 catttggtt cattctctg ctctg 25

 <210> 369
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 369
 aaaaactcag aacaactcat ttgcacc 28

 <210> 370
 <211> 41
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-41
 <223> Synthetic construct.

 <400> 370
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

 <210> 371
 <211> 1150
 <212> DNA
 <213> Homo sapiens

 <400> 371
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gaattcggct cgaggctggt ggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccgctgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc gggcgagcgg ctgccgggcc gggactggtg cgcgagggcg 200
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 tcaactgctc ggaaccagca ggtggttacc ttgtccctgt cacagcgcca 350
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<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1					5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys	
				20					25					30	
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	
				35					40					45	

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60
 Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75
 Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90
 Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105
 Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120
 Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135
 Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165
 Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180
 Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195
 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210
 Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225
 Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240
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 260 265

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

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aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

gccctggaga tgggtcccg gcgcggggc tgggtgtgtc tegtgtctg 100

gctccccgcg tgcgtcgcgg ccacggcctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200

cctgccaagc actttgggtg tatctttcac acaaggtatg agcagatcca 250

ccttgtcccc gctgaacctc cagaggcctg cygggaactc agcaacggtt 300
 tcttcaccca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcggggggg cggtagcatc 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatecccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtc atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcgtt gctaggctga aagggaaagcc acaccactgg ccttccttc 800
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggct tctggctaga accgaaaca aaaggagctg aaggcagggt 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu	1	5	10	15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu	20	25	30	
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr	35	40	45	
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr	50	55	60	
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly	65	70	75	
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val	80	85	90	

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccaggcg gatactgaac 100
 ctgaacaaga tggtaagca agtgactggg aaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagaccatg actgctgta tgaccacctg 250
 aagaccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tggtaagca agtgactggg aaatgccca tcttc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt cttctggat gggggcccag gggggcccag agagtataaa 50
ggcgaagtgg aggggtcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cagccttgcc 150
ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctgggtaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata ccagggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
cttctctccg gggatgggtc atgtacacca gcaaggaccg ctatttctat 450
tttgggaagc ttgatggcca gatctcctct gcctacccca gccagagggg 500
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcataaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctagggtgg 650
gggatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15
Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 50 55 60
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
 65 70 75
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 80 85 90
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 95 100 105
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110 115 120
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 125 130 135
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 140 145 150
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 155 160 165
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 170 175

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagccccc aaattgctgga agaatacatc 150
 atgttttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccga cccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgcg cggaatgcgg 300
 tgttgggatt tatttgttct tggagtggtc tgcgtggctg gcaaagaata 350
 atgttccaaa atcggtccat ctcccagggt gtcgaatttt tcttctcggg 400
 tgtcagcgag ccctgactca ctacagtcca gctgacaggg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
 cactgtttat agccccact gtcttactga caatgctttc tctgcccga 600
 cgaggatgcc ctaagggtcg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactctgt ggttgcttag 700
 gtttgtccct tcgtataaac agccttcaaa aacttaagta taatcaattt 750
 aaagggtca accagctcac ctggctatac ctggaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttcgggaa gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttgacctt gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaaggtt ggtcagcctt 1200
 cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250
 gtccctgacc tggagctcct tacaagggtc tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggaccc agtgttttcc agtgtgtccc gaatctgcag 1350
 cgctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatattgc tcccttgtaa actggctgaa aagttttaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaag agctgcaagg 1550
 agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggtcc tcccaaagcc gacgtttta 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgac 1700
 ggtgggagcc acagagcccg gccagagac cgaatgctgac gccagcaca 1750
 tctctttcca taaaatcacc gcgggcagcg tggcgctttt cctgtccgtg 1800
 ctgctatcc tgcgtgttat ctacgtgtca tggaaagcgt accctgcgag 1850
 catgaagcag ctgcagcagc gctccctcat gcgaagcgc aggaaaaaga 1900
 aaagcagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggag 2000
 gggacctgc acctataaca aatcggtctc cagggagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtcttta 2100

ttgaactctg gtgactatca agggaaacgog atgccccccc tccccttccc 2150
 tctccctctc actttgggtg caagatcctt ccttggtcgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact cgggtttaat ataataccta 2300
 ttgtataaga ccttttactg attccattaa tgcgcattt gttttaagat 2350
 aaaactttct tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Ser	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

	200		205		210
His Leu Glu His	Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu	Phe		
	215	220	225		
Pro Arg Leu Val	Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys			
	230	235	240		
Ile Ser Val Ile	Gly Gln Thr Met Ser Trp	Thr Trp Ser Ser Leu			
	245	250	255		
Gln Arg Leu Asp	Leu Ser Gly Asn Glu Ile	Glu Ala Phe Ser Gly			
	260	265	270		
Pro Ser Val Phe	Gln Cys Val Pro Asn Leu	Gln Arg Leu Asn Leu			
	275	280	285		
Asp Ser Asn Lys	Leu Thr Phe Ile Gly Gln	Glu Ile Leu Asp Ser			
	290	295	300		
Trp Ile Ser Leu	Asn Asp Ile Ser Leu Ala	Gly Asn Ile Trp Glu			
	305	310	315		
Cys Ser Arg Asn	Ile Cys Ser Leu Val Asn	Trp Leu Lys Ser Phe			
	320	325	330		
Lys Gly Leu Arg	Glu Asn Thr Ile Ile Cys	Ala Ser Pro Lys Glu			
	335	340	345		
Leu Gln Gly Val	Asn Val Ile Asp Ala Val	Lys Asn Tyr Ser Ile			
	350	355	360		
Cys Gly Lys Ser	Thr Thr Glu Arg Phe Asp	Leu Ala Arg Ala Leu			
	365	370	375		
Pro Lys Pro Thr	Phe Lys Pro Lys Leu Pro	Arg Pro Lys His Glu			
	380	385	390		
Ser Lys Pro Pro	Leu Pro Pro Thr Val Gly	Ala Thr Glu Pro Gly			
	395	400	405		
Pro Glu Thr Asp	Ala Asp Ala Glu His Ile	Ser Phe His Lys Ile			
	410	415	420		
Ile Ala Gly Ser	Val Ala Leu Phe Leu Ser	Val Leu Val Ile Leu			
	425	430	435		
Leu Val Ile Tyr	Val Ser Trp Lys Arg Tyr	Pro Ala Ser Met Lys			
	440	445	450		
Gln Leu Gln Gln	Arg Ser Leu Met Arg Arg	His Arg Lys Lys Lys			
	455	460	465		
Arg Gln Ser Leu	Lys Gln Met Thr Pro Ser	Thr Gln Glu Phe Tyr			
	470	475	480		
Val Asp Tyr Lys	Pro Thr Asn Thr Glu Thr	Ser Glu Met Leu Leu			
	485	490	495		

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gtcgagtta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacaCagg caccaaacca ctatcctaag 50

ttgactgtcc tttaaataatg tcaagatcca gacttttca_g tgtcacctca 100

gcgatctcaa cgatagggat cttgtgttg ccgctattcc agttggtgct 150

ctcgagccta ccatgccaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctgggat atctggatcc tctgctgct ggttttgggtg 250
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
 gagaccccca attgattctc acaggcgac catggcagtt tttgctgttg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
 ggaattcacc tccaactca aacccttgac ctatatcctg ttcctgctcc 450
 atgttttggc cctttaggct cccacacctc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaa 650
 ggatgttgga aaaaattttg gtcatggaga tgtttaaata gtaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaacca 750
 ataatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttaa actctttcct agcatggggt ccataaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100
 ttagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaaaaa aatttcccct tttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggttgc gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatctttag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1					5				10					15

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Val	Leu		
			50					55						60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65					70						75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
			80					85						90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95					100						105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110					115						120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125					130						135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140					145							

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtg tcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

cctaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 393
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<210> 394
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 394
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 gagcagctg acgcccgtt attagctctc gctgcgtgc cccggctcag 150
 aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
 tctcttttac ttgggagag agagaaagtc agatgccctt ttaaaactcc 250
 ctcttcaaaa ctcatctcct gggtgactga gtaataagag tggatacaac 300
 cttgctgaag atgaagaata tacaatattg aggatatttt ttcttttttt 350
 ttttcaagtc ttgatttgtg gcttacctca agttaccatt ttccagtcaa 400
 gtctgtttgt ttgctcttc agaaatgttt ttacaatct caagaaaaaa 450
 tatgtccag aaattgagtt tactgttgct tgtatttggg ctcaattggg 500
 gattgatgtt actgcactat acttttcaac aaccaagaca tcaagcagt 550
 gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
 tctagcagag gaaaataaga acacagtgga gtgcgagaac ggtgcttcta 650
 tggcaggata tgccgatctg aaaagaacaa ttgctgtcct tctggatgac 700
 attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
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 aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtgg 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
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agtataatac acgttttttg gacaagtga gaattgttaa tcattctgtc 1250
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tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
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actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200
catgtagcaa taattacaat attttattaa aataaatatg tgaatatattg 2250
tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300
acctttatgt gaagaaatta atttatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
1 5 10 15

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

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 accttcggcc ttctcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat cctctgagac acagcccaact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttgccg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
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 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
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 tgccaggggc cccaccatct tgtgacaaat ggtgtggccc agggccacat 1150
 aacagactgc tgtcctgggc tgccctcagg cccgagtaac ttatgttcaa 1200
 tgtgccaaca ccagtgggga gcccgaggc ctatgtggca gcgtcacacc 1250
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25				30	
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40				45	
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55				60	
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70				75	
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85				90	
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95					100				105	
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110					115				120	
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125					130				135	
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145				150	

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
 155 160 165
 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
 170 175 180
 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
 185 190 195
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
 200 205 210
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
 215 220 225
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
 230 235 240
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
 245 250 255
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
 260 265 270
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
 275 280 285
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
 305 310 315
 Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
 320 325 330
 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
 335 340 345
 Ala Ala Arg Gly Pro Thr Ile Leu
 350

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.
 <400> 399
 ggttggtgcc cgaaaggtcc agc 23
 <210> 400
 <211> 44
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.
 <400> 400
 caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44
 <210> 401
 <211> 1571
 <212> DNA
 <213> Homo sapiens
 <400> 401
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 gaggtctatc gcgtcaattc cccaaaacaa gtttgacat tccccctgaa 150
 atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200
 ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250
 cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300
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 ccateccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
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 ccaaaaaaaaa aaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20						25					30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40						45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
			50					55						60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65					70						75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80					85						90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Trp
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
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<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

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<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
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aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgc tcggttg 200
ggagacgggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgcct ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccttttg aaatcagtca ttggagggat gatggctggt gttattggcc 450
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ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
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gctgggtacc caatatacaa agagcagcac tgg tgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgtct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggtgttc aaggtgaagg atcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgacct ctggtcaat ggtgttctg 950
cttacttatg aaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

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Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr		35	40	45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp		50	55	60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala		65	70	75
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly		80	85	90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg		95	100	105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser		110	115	120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met		125	130	135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu		140	145	150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly		155	160	165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile		170	175	180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro		185	190	195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr		200	205	210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu		215	220	225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu		230	235	240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg		245	250	255
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr		260	265	270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly		275	280	285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met		290	295	300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg				

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcggaatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggaacgctg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaâtg gcaggcttcc 150
tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgtcgcâggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcagt 350
ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400
ctgtttagga agaacagggtg ctcgagttag gcttttcatt ggtttcatgt 450
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggtgcatat 500
gttacccaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttctt tttgttata 650
 tctgtttgta gataggTTTT ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatgtt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttcttttatt ttcattgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag gggtacatca 900
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacgggtg 950
 gctcatgcct gtaatccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaaac cgggggggcag 1150
 aggttgagtg gagctgagtt tgccccactg cactctagcc tgggggagaa 1200
 agtgaactc cctctcaaaa aaaagaccac tctcagatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaagggt ttacagcaag ttgtaactta tttggccta aaaatgaggt 1350
 ttttttggtt aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccgaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1				5					10				15	
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
			20						25				30	
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
			35						40				45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
			50						55				60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
			65						70				75	

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
 80 85 90
 Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
 95 100 105
 Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
 110 115 120
 Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
 125 130 135
 Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
 140 145 150
 Gly Arg Thr Glu Glu Leu Trp Thr
 155

 <210> 411
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 411
 gtttgaggaa gctgggatac 20

 <210> 412
 <211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 412
 ccaaaactga gcacctgttc 30

 <210> 413
 <211> 40
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

 <400> 413
 atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

 <210> 414

<211> 1337
 <212> DNA
 <213> Homo sapiens

<400> 414
 gtgatggca aacttctca aaggaggggc agagcctgcy cagggcagga 50
 gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
 actgcatcta gagaggggcc gtctgtgagg ccactacccc tccagcaact 150
 gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
 gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
 aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
 acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcacc 350
 ttgtccatag tcacgacatg gatgtttatt cgaagctaca tgagctttag 400
 catgaaaacc atccgtctgc cagctgggct ggcagcctcg cccaccaagg 450
 agatccaggt taaaagtac aagtgtggcc tcatcaagcc ctgccagcc 500
 aactactttg cgttttaaat ctgcagtggg gccccaacg tcgtgggccc 550
 tactatgtgc ttgaagacc gcatgacatc gagtctgtg aaaacaatg 600
 tgggcaagag cctaaacatc gccctggtga atggaaccac gggagctgtg 650
 ctgggacaga aggcatttga catgtactct ggagatgta tgacacctag 700
 gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750
 acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800
 gacttgggga gttcctacgc aaaacaactg ggctccggg acagctgggt 850
 ctcatagga gccaaagacc tcaggggtaa aagcccttt gagcagttct 900
 taagaacag cccagacaca aacaatacag agggatggcc agagctgctg 950
 gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000
 ttctcagcc aggggcctga agaagctcct gcctgactta ggagtacagg 1050
 ccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100
 gcaggtcctt gcacgctgtg tcgcctctct cctcctcga aacagaaccc 1150
 tcccacagca catcctaccc ggaagaccag cctcagagg tcctcttgga 1200
 accagctgtc tgtgagaga atggggtgct ttctcaggg actgctgacg 1250
 gctggtcctg aggaaggaca aactcccag acttgagccc aattaaattt 1300
 tatttttgct ggttttgaaa aaaaaaaaa aaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
 <223> Synthetic construct.

 <400> 416
 gccatagtcg cgacatggat g 21

 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 417
 ggatggccag agctgctg 18

 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 418
 aaagtacaag tgtggcctca tcaagc 26

 <210> 419
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 419
 tctgactcct aagtcaggca ggag 24

 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 420
 attctctcca cagacagctg gttc 24

<210> 421
 <211> 46
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-46
 <223> Synthetic construct.

 <400> 421
 gtacaagtggt ggcctcatca agccctgccc agccaactac tttagcg 46

 <210> 422
 <211> 1701
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> unsure
 <222> 1528
 <223> unknown base

 <400> 422
 gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
 tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
 tggaaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
 caccgccagga gctcgctcgc tctctctctc tctctctcac tctctccctc 200
 ctctctctct gctgtgctta gtctcttagt cctcaaattc ccagtccctc 250
 gcaccctctc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
 atttgatcc tggctgcaga tgggggtcaa cactggacgt atgaggggccc 350
 acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
 cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
 ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
 ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550
 tgtatctggg tggacttccc cgaaaatatg tagctgccca gctccacctg 600
 cactgggggtc agaaaggatc ccaggggggg tcagaacacc agatcaacag 650
 tgaagccaca tttagcagagc tccacattgt acattatgac tctgattcct 700
 atgacagctt gagttaggct gctgagaggc ctacgggcct ggctgtcctg 750
 ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
 tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtcg 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
 cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
 gacagttttt tatagaaggt ccagatttcc aatggaacag ctggaaaagc 1000
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctgcta 1050
 cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
 ttctacccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgtaggaat cttggttggc tgtctctgcc ttctctggc tgtttatttc 1200
 attgctagaa agattcgaa gaagaggctg gaaaaccgaa agagtgtggt 1250
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
 catgtagtg gatgacttcc ctcatgcct atcaggaagc ctctaaaatg 1350
 ggggttagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
 ccttccccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
 gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtctctta cccctcact tttatggccc 1600
 ttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
 gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

Met	Leu	Phe	Ser	Ala	Leu	Leu	Leu	Glu	Val	Ile	Trp	Ile	Leu	Ala
1				5					10					15
Ala	Asp	Gly	Gly	Gln	His	Trp	Thr	Tyr	Glu	Gly	Pro	His	Gly	Gln
				20					25					30
Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
				35					40					45
Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
				50					55					60
Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
				65					70					75
Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu		Pro	Arg	Lys	Tyr	Val	Ala				
				95						100					105				
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
				110					115					120					
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
				125					130					135					
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
				140					145					150					
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
				155					160					165					
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
				170					175					180					
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
				185					190					195					
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
				200					205					210					
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
				215					220					225					
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
				230					235					240					
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
				245					250					255					
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
				260					265					270					
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
				275					280					285					
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
				290					295					300					
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
				305					310					315					
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
				320					325					330					
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
				335															

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 424
 gtaaaagtcgc tggccagc 18

 <210> 425
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 425
 cccgatctgc ctgctgta 18

 <210> 426
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 426
 ctgcactgta tggccattat tgtg 24

 <210> 427
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 427
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

 <210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

 <400> 428
 aattttttcac cagagtaaacc ttgagaaacc aactggacct tgagtattgt 50

 acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100

 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aactctcttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
ctaccaaacc aacagcagtc aaatcagggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaact 300
ctgctgcagg aatgacacct ggtaccaga cccaccatt gacctggga 350
gggttgaatg tacaacagca actgcacca catgtgttac caattttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgttccggg aggcatactg 500
cccaccagtc aggcaggggc taatccagat gtcaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcagccc 600
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gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagtctgct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgtctgct ggatgatatg catattaaaa catattttga aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5					10					15
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
			20						25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Ser	Asn	
			35						40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
			50						55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
			65						70					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80						85				90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
 ggagagaggc gcgcgggtga aagcgccatt gatgcagcct gcgcgggcct 50
 cgagcgcgcg cgagaccaga cgctgaccac gtctctctcc tcggtctcct 100
 ccgcctccag ctccgcgctg ccgcgcagcc gggagccatg cgacccacagg 150
 gcccgcgcgc ctcccgagcg cggtctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgcgctc gagcgccctct gagatcccca aggggaagca 250
 aaagcgcgag ctccgcgaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttatct cggtacacc tgggatccca ggctgggatg gattcaaaag 400
 agaaaagggg gaatgtctga gggaaagcct tgaggagtcc tggacacca 450
 actacaagca gtgttcatgg agttcattga attatggcat agatcttggt 500
 aaaattgctg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgtctgc 600
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attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
 aattaatatt catcgcaatt cttctgtgga aggactttgt gaaggaattg 750
 gtgctggatt agtggatggt gctatctggg ttggcaattg ttcagattac 800
 ccaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
 tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
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 tccaaca 1257

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<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

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Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
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<210> 472

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